

Modifying the control of gene expression
behavior by the deletion of connectrons and
by the design and addition of synthetic
connectrons in prokaryotic, archea and
5 eukaryotic genomes

Reference to Related Application

The present application includes the subject of Provisional
Application Serial No. 60/393,558 filed July 5, 2002

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The present application is a continuation in part of US Patent
Application Serial Number 09/866,925 filed May 30, 2001 entitled
ALGORITHMIC DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL
THE EXPRESSION OF SETS OF GENES IN PROKARYOTIC, ARCHEA AND
15 EUKARYOTIC GENOMES

15

The present application is also related to US Patent Application
Serial Number 10/339,666 filed January 10, 2003 entitled
SIMULATION OF GENE EXPRESSION CONTROL USING CONNECTRONS,
20 INTERFERENCE RNAS (IRNAS) AND SMALL TEMPORAL RNAS (STRNAS) IN
PROKARYOTIC, ARCHEA AND EUKARYOTIC GENOMES

20

The present application is also related to US Patent Application
Serial Number 10/364,516 filed February 12, 2003 entitled
25 DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE
EXPRESSION OF SETS OF GENES IN THE ESCHERICHIA COLI K-12 MG1655
COMPLETE GENOME

25

The present application is also related to US Patent Application
Serial Number 10/364,412 filed February 12, 2003 entitled
DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE
EXPRESSION OF SETS OF GENES IN THE SACCHAROMYCES CEREVISIAE
5 COMPLETE GENOME

The present application is also related to US Patent Application
Serial Number 10/299,056 filed November 19, 2002 entitled
DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE
10 EXPRESSION OF SETS OF GENES IN THE HALOBACTERIUM SP. NRC-1
COMPLETE GENOME

The present application is also related to US Patent Application
Serial Number 10/367,832 filed February 19, 2003 entitled
15 DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE
EXPRESSION OF SETS OF GENES IN THE PSEUDOMONAS AERUGINOSA PA01,
COMPLETE GENOME

The present application is also related to US Patent Application
20 Serial Number 10/287,818 filed November 5, 2002 entitled
DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE
EXPRESSION OF SETS OF GENES IN THE VIBRIO CHOLERAЕ CHROMOSOME I,
COMPLETE CHROMOSOME

25 The present application is also related to US Patent Application
Serial Number 10/305,275 filed November 27, 2002 entitled
DETERMINATION OF FLANKING DNA SEQUENCES THAT CONTROL THE
EXPRESSION OF SETS OF GENES IN THE AEROPYRUM PERNIX K1 COMPLETE
GENOME

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Introduction

The connectron structure of a genome determines sets of four DNA sequences of minimum length of 15-bases (C1 and C2 which are in the 3'UTR of a gene, T1 which is on the 5'-side and T2 which is on the 3'-side of a set of genes). The connectrons in a genome control the expression of sets of genes. Each native genome has a particular set of connectrons that control the expression of sets of genes in many different ways. The gene expression behavior can be changed by deleting existing connectrons and by adding new connectrons that have been designed to achieve specific new gene expression patterns. This patent application describes the invention of methods for deleting connectrons as well as the invention of four classes of synthetic and designed connectrons that can be used to modify the connectron behavior of a genome. In addition this application describes the invention of four methods that implement synthetic connectrons with differing proportions of novelty.

Definitions

20

Double stranded DNA - Watson and Crick showed in 1953 that DNA naturally forms a double-stranded helix. A typical double stranded sequence is

25 5'-TAGAGGAGTACCAC-3'
 3'-ATCTCCTCATGGTG-5'

Hydrogen Bond - The force between a hydrogen atom and another heavier atom such as Oxygen (O), Nitrogen (N), Phosphorus (P), or Sulfur (S).

- 5 **Positive strand** - The positive strand is normally represented 5' to 3' running left to right as in

5'-TAGAGGAGTACCAC-3'

- 10 **Negative strand** - The negative strand is normally represented 5' to 3' running right to left as in

3'-ATCTCCTCATGGTG-5'

- 15 **Single stranded RNA** - Either the positive or the negative strand of the double-stranded DNA can be transcribed by the polymerase. In RNA U replaces T.

RNA of positive strand sequence 5'-UAGAGGAGUACCAC-3'

- 20 RNA of negative strand sequence 5'-GUGGUACUCCUCUA-3'

Antisense RNA - The antisense strand of any RNA sequence is the complement sequence

- 25 RNA sequence 5'-UAGAGGAGUACCAC-3'
Antisense RNA sequence 3'-AUCUCCUCAUGGUG-5'

Triple Strand Helix - The RNA sequence of a RNA/DNA triple-strand complex is the same as the positive strand of the DNA

30

DNA positive strand 5'-TAGAGGAGTACCAC-3'
DNA negative strand 3'-ATCTCCTCATGGTG-5'

RNA strand

5'-UAGAGGAGUACCAC-3'

Promoter - Any region of DNA, that binds proteins which engage the polymerase transcription mechanism.

5

TATA Box - A region near the 3' end of a promoter with the sequence TATA.

10 **mRNA** - The RNA produced from the DNA by the polymerase as a result of transcription

Start of transcription - The 3' end of a promoter where the polymerase mechanism begins to transcribe DNA into mRNA.

15 **Exon** - Any region of mRNA which is used to code for proteins

Intron - Any region of mRNA lying between two exons which is not used to code for proteins. The introns are edited out of the initial RNA transcript to form the mature mRNA.

20

3' UTR - The untranslated 3' end of an mRNA is beyond the end of the last exon. A stop codon in the mRNA causes the ribosome to stop the translation of mRNA into protein.

25 **End of translation** - The 3' end of the 3'-most exon.

Translated region - Any collection of exons and introns.

30 **Gene** - Any DNA region that codes for a protein. Introns do not occur in prokaryotic genes and they sometime fail to occur in eukaryotic genes. A typical model of a gene is

```

|<-----Promoter----->|
      |<-TATA Box->|
                |<-Beginning of Translation
                |<-----Translated Region----->|
5      End of Translation->|
|<-Exon->|<-Intron->|<-Exon->|<-Intron->|<-Exon->|<-3' UTR->|
+ strand -----
- strand -----
10 |<-----Gene----->|

```

Positive strand gene - Any gene in which the features run 5' to 3' on the positive strand

15 **Negative strand gene** - Any gene in which the features run 5' to 3' on the negative strand

C1 sequence - Any positive or negative strand DNA sequence of 15 bases or more. The C2 sequence must occur in the same
20 chromosome as the C1 sequence.

C2 sequence - Any positive or negative strand DNA sequence of 15 bases or more. The C1 sequence must occur in the same
25 chromosome as the C2 sequence.

C1/C2 - Any positive or negative strand DNA sequence of 40 or more bases such that the C1 sequence is adjacent to the C2 sequence

30 **T1 sequence** - Any positive or negative strand DNA sequence of 15 bases or more that is on the same chromosome as the T2 sequence. The T1 and T2 sequences must be between about 1kb and 105kb apart.

T2 sequence - Any positive or negative strand DNA sequence of 15 bases or more that is on the same chromosome as the T1 sequence. The T2 and T1 sequences must be between about 1kb and 105kb apart.

5

Last exon gap or **Gap-Distance** - The number of bases between the end of transcription and the beginning of the C1/C2 sequence. In prokaryotes and single-celled eukaryotes this gap can range from no bases to 500 bases. In multi-celled eukaryotes the gap
10 can be as large as 10,000 bases.

Poly-adenylation signal - A number of Adenosine (A) bases are added to the mRNA at the end of the 3'UTR.

15 **Possible Connectron** - Any set of T1, T2 and C1/C2 sequences such that the C1 sequence is identical to the T1 sequence and the C2 sequence is identical to the T2 sequence. The promoter of some gene causes the mRNA of the gene to be expressed. The mRNA is edited to eliminate the introns. The whole mRNA including the
20 3'UTR can move about in the cell or the nucleus of the cell. The C1/C2 RNA that is part of the 3'UTR moves to the T1 and T2 DNA sequences. A triple-stranded complex of the DNA and the RNA forms such that the C1 sequence forms hydrogen bonds with the T1 sequence and the C2 sequence forms hydrogen bonds with the T2
25 sequence. Because the C1 sequence is adjacent to the C2 sequence, the T1 sequence is brought physically close to the T2 sequence. This produces a loop of between about 1kb and 105kb in the DNA. Histone proteins reduce the length of the DNA by binding 200 bases. Histone/DNA complexes form six-fold symmetry
30 chromatin assemblies. The diameter of the chromatin assemblies is approximately 30nm.

Real Connectron - Any Possible Connectron which is within the Gap-Distance of some gene

5 **Homologous connectron** - The T1 sequence and the T2 sequence are on the same chromosome as the C1/C2 sequence

Heterologous connectron - The T1 sequence and the T2 sequence are on a chromosome different from chromosome of the C1/C2 sequence

10

Permanent connectron - Any C1/C2 sequence, which is 3' UTR to some gene that is not surrounded by any T1 and T2 sequence pairs

15 **Transient connectron** - Any C1/C2 sequence, which is 3' UTR to some gene that is surrounded by one or more T1 and T2 sequence pairs

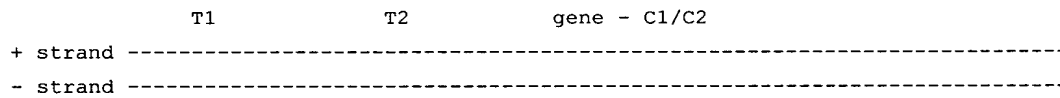
20 **One-shot or Self-limiting connectron** - Any C1/C2 sequence which is 3'UTR to some gene that is surrounded by the T1 and T2 sequences such that C1=T1 and C2=T2

25 **Geneless connectron** - Any C1/C2 sequence that is not 3'UTR to some gene but is surrounded by some T1 and T2. A promoter may lie 5' to the C1/C2 sequence.

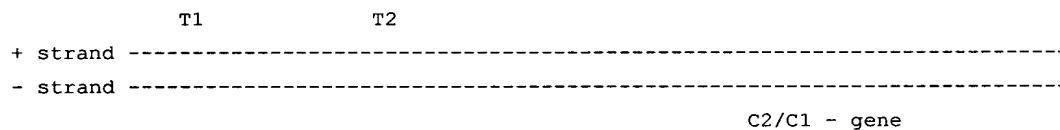
30 **Bi-directionality of Connectron Excitation** - A C1/C2 short loop on one strand selects a T1-T2 long loop pair on the same or the opposite strand. The C1/C2 short loop has a complementary C1'/C2' sequence on the opposite strand. Similarly the T1-T2 long loop pair has a complementary long loop pair T1'-T2'. Wherever a C1/C2, T1-T2 tetrad exists there is a complementary C1'/C2', T1'-T2' tetrad. The C1/C2 short loop can be

transcribed as a 3'UTR to a gene on the same strand. The C1'/C2' short loop which is on the strand opposite to the C1/C2 short loop can also be transcribed as a 3'UTR to a gene on the same strand. There are four possible models of action

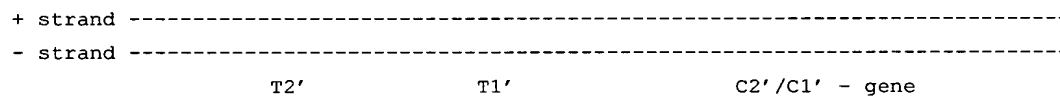
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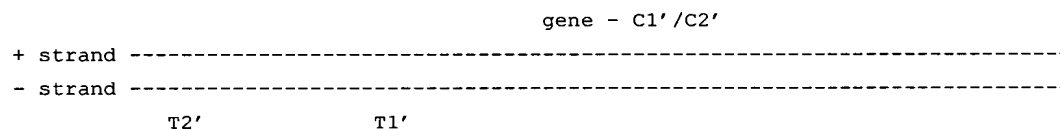
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25

Of course, the short loops and the long loops do not have to be on the same chromosome.

Hierarchy of connectron action - When a C1/C2 is expressed it forms a T1-T2 loop by forming a connectron. The C1/C2 sequence does not have to be on the same chromosome as the T1 and T2 sequences. This provides a way of causing interaction between chromosomes. When the T1-T2 loop forms, any genes in that loop region which had been expressing C1/C2 sequences in their 3'UTRs, now cease expressing the C1/C2 sequences. The connectrons formed by these C1/C2 sequences will cease to exist after some time thus opening up the genes inside the respective T1-T2 loops to expression. The hierarchy of connectron action

is alternates between repression and expression. The connectron hierarchies can be of any depth.

One-to-Many connectron action - One C1/C2 sequence can form

5 connectrons in many different places on many different chromosomes. The only requirement is that C1=T1 and C2=T2. This makes it possible for one expression event to control the expression of many genes on different chromosomes.

10 **Many-to-One connectron action** - C1/C2s that come from many different places on many different chromosomes can form a connectron for a specific T1-T2 sequence pair. The only requirement is that C1=T1 and C2=T2. This makes it possible for many different expression events to control the expression of
15 one set of genes on a particular chromosome.

Many-to-Many connectron action - The arrangement of C1/C2s and T1-T2s across chromosomes can form a complex web of gene expression control relationships.

20

Percentage of the Genome Regulated by Connectrons - Since the connectrons for a sequenced genome can be calculated, the percentage of the genome that is open to connectron regulation can be known.

25

Emergent Property - The network of connectrons in any genome emerges from a knowledge of the complete DNA sequence of the genome. Because both the C1/C2 sequences and the T1-T2 sequences can be any place in the genome, the whole genomic
30 sequence must be known before all the connectrons can be determined.

Paradigm Shift - For the past fifty years since the discovery by Watson and Crick of the double-helical nature of DNA, the reigning paradigm for scientific discovery has been the study of one gene and its effects on the behavior of a cell. The advent
5 of genomic sequencing and this invention of connectrons that emerge from the whole genome will produce a shift in the way scientists view biological systems and the way they formulate and execute experiments. The many-to-many relationships between the connectrons mean that there are many ways in which the
10 expression of a set of genes can be modulated. The multiplicity of control pathways produces a system stability that makes it possible for biological systems to be stable for long periods of evolutionary time. The thinking that goes into formulating scientific experiments will have to change to accommodate the
15 changes in understanding that will be induced by the application and extension of this patent application.

20 **Sequence Element** - The double-stranded sequence of either a C1, a C2, a T1 or a T2 of some connectron.

Native Sequence Element - Any sequence element of a connectron which is a constitutive part of the native genome.

25

Native Connectron - Any connectron in which all four (i.e. the C1, C2, T1 and T2 sequence) sequence elements are constitutive parts of the native genome.

30 **Synthetic Sequence Element** - Any sequence element that has been added into a genome at some particular place. The actual sequence of bases may occur in one or more places in the genome.

The synthetic aspect is that an instance has been placed into the genome at a specific place by design.

5 **Copied Sequence Element** - Any sequence element that has been copied from one place in a genome to another place in that genome.

10 **Unique Sequence Element** - Any double-stranded DNA sequence element for which there is only one pair of instances. Such a pair of instances can be used to implement the C1 and T1 synthetic sequence elements of a connectron or the C2 and T2 synthetic sequence elements of a connectron.

15 **Extracted Sequence** - Any sequence element that is moved from one place in a genome to another place in the same genome. The moved sequence element can be unique or non-unique.

20 **Synthetic Connectron** - Any connectron in which one or more of the sequence elements in a native connectron are substituted by synthetic sequence elements.

Designed Connectron - Any connectron that does not exist in the native genome.

25 **RNA-Based Connectron** - Any connectron in which the C1 and C2 elements are generated as RNA in the 3'UTR of some gene.

30 **DBP** - A multi-domain zinc-finger DNA Binding Protein that binds to a specific DNA double-stranded sequence.

Protein-Based Synthetic Connectron - Any synthetic connectron in which the C1 and C2 elements are generated by a DBP.

PNA - A Peptide Nucleic Acid is a molecular construct patented and supplied by Boehringer-Mannheim. The A, T, G, C base portions of are the same as an RNA but the ribose ring has been
5 replaced by a peptide-like configuration of atoms.

PNA-Based Synthetic Connectron - Any synthetic connectron in which the C1 and C2 elements are generated by a sequence of Peptide Nucleic Acid (PNA) bases.

10

Generalized Synthetic Connectron - Any synthetic connectron in which the C1 and C2 elements are generated by two linked double-strand DNA binding elements.

15 **Individual Connectron State** - A binary representation of whether the C1-C2 elements are bound to the cognate T1 and T2 elements. A 0 means that the connectron is not formed. A 1 means that the connectron is formed and hence the expression of the genes between the T1 and T2 elements are turned off.

20

Genomic Connectron State - The collection of all the individual native and synthetic connectron states in a genome. The individual connectron states are ordered along each chromosome and plasmid by the position of the T1 element.

25

Connectron Simulation - The temporal transitions of the genomic connectron states as the individual connectron states interact with each other.

Content of the CD

The Sequence Listing Part is incorporated herein by reference.

The material contained on this compact disc attached hereto was
5 created on 6/30/03,

synthetic.sequences has 13,770 bytes

Brief Description of the Objects of the Invention

The basic methods patent application provides the methods for
5 determining the structure of the native connectrons in a variety
of genomes. Since the original conceptualization of connectrons
followed from the work that we did on the design of zinc-finger
DNA Binding Proteins (DBPs), US Patent 6,205,404, it has always
been the applicant's intention to use these designed proteins to
10 modify genomic connectron behavior.

An object of this invention is to provide a method for utilizing
the genomic simulation of connectron behavior to facilitate the
optimization of design decisions related to deleting connectrons
15 from a genome or adding connectrons to a genome.

An object of this invention is to provide a method for utilizing
the genomic simulation by computer of connectron behavior to
facilitate the optimization by computer of design decisions
20 related to deleting connectrons from a genome or adding
connectrons to a genome.

An object of this invention is to provide a method for modifying
the connectron behavior of a genome by deleting and adding
25 connectrons.

An object of the invention is to provide a method for creating
new connectrons in a genome by copying one or more double-
stranded DNA sequence elements from one place in the genome to
30 another place in the genome or by extracting a double-stranded
DNA sequence element from one place in the genome and moving it

to another place in the genome or by introducing a new unique pair of double-stranded DNA sequence elements into the genome at specific places.

- 5 An object of the invention is to provide a method for creating new connectrons in a genome by copying, extracting or adding unique DNA elements in addition to using either DBPs, PNAs or a linked pair of generalized DNA binding elements to implement the C1 and C2 elements of the new connectron.

10

Description of the Tables

- 5 Table 1 - The 10 possible ways of deleting a connectron
- Table 2 - The 15 possible synthetic connectrons defined by combinations of native and synthetic elements
- 10 Table 3 - The 4 possible synthetic connectrons defined by combinations of native and synthetic DNA elements and synthetic DBP elements
- 15 Table 4 - The 4 possible synthetic connectrons defined by combinations of native and synthetic DNA elements and synthetic PNA elements
- 20 Table 5 - The 4 possible synthetic connectrons defined by combinations of native and synthetic DNA elements and a pair of linked double-strand DNA binding elements
- Table 6 - The 2 possible ways of implementing a single synthetic element in a synthetic connectron
- 25 Table 7 - The 14 possible ways of implementing a pair of synthetic elements in a synthetic connectron
- Table 8 - The 41 possible ways of implementing three synthetic elements in a synthetic connectron
- 30 Table 9 - The 25 possible ways of implementing four synthetic elements in a synthetic connectron

Description of the Invention

The simulation of the connectron behavior of a genome provides a powerful way of understanding how individual connectrons
5 interact with each other. From the more than 100 genomes whose connectron structure we have determined, it is clear that a given C1-C2 may generate many different connectrons - the one-to-many connectron action mode. Similarly it is clear that a given connectron may be generated by the expression of many
10 different instances of the C1-C2 signal - the many-to-one connectron action mode. The temporal interaction of these one-to-many and many-to-one modes of connectron control of gene expression can best be understood by doing a genomic connectron simulation and looking at the results. This is especially
15 important when determining when and where to delete connectrons from a native genome or add new connectrons to a native genome. Genomic connectron simulation is the subject of a related patent application.

20 Although there are instances in different genomes of a C1-C2 generating only one connectron, much more frequently a given C1-C2 will generate several connectrons. When only one connectron is generated by a given C1-C2, a decision to delete the connectron or to add another connectron using the same or
25 different C1 or C2 elements will have no side effects as long as the T1 and T2 elements are only used by this connectron. This is the relative infrequent example of one-to-one. Much more frequently, deleting or changing a given C1 or C2 may have multiple consequences and serious behavioral side effects.

30 Modification of genomic connectron control of gene expression will inevitably involve compromises, design decisions, and -

worst of all - patch-ups. Consider an example in which a given C1-C2 generates two connectrons. For some reason we desire to delete one of the two connectrons. A patch-up can be achieved by finding some other way to generate the second connectron.

- 5 This could be achieved by adding one or more synthetic connectron elements to generate the second connectron as a synthetic connectron.

10 If there are no side effects of a design decision then that is the optimum. If there are side effects, the genomic simulation of connectron behavior makes it possible to evaluate the genomic behavioral consequences of the design and implementation decisions.

- 15 The deletion of a connectron as shown in table 1 can occur in 10 different ways ranging from deleting or modifying just one sequence element to deleting or modifying all four sequence elements. Anything that destroys the sequence recognition of the T1 by the C1 or the T2 by the C2 will have the effect of
20 deleting the connectron.

Any or all of the four elements (C1, C2, T1 and T2) of a native connectron can be replaced with synthetic elements to form a synthetic connectron. Table 2 gives the 15 possible types of
25 synthetic connectrons. A designed connectron can be introduced into a genome to either (1) control the expression of a set of genes already controlled by other native connectrons, or (2) control the expression of a newly selected set of genes. Using DNA sequences, a designed connectron be made from any of the 15
30 combinations of native and synthetic elements in Table 2. If the C1 and C2 elements of a connectron are generated by a zinc-finger DBP then the 4 combinations of synthetic and designed

connectrons in table 3 are possible. If the C1 and C2 elements of a connectron are generated by a PNA then the 4 combinations of synthetic and designed connectrons in table 4 are possible. If the C1 and C2 elements of a connectron are generated by a
5 linked pair of DNA binding elements then the 4 combinations of synthetic and designed connectrons in table 5 are possible. The DNA binding elements G1 and G2 can be proteins or any other molecular material that recognizes the DNA sequences of the T1 and T2 elements.

10

The implementation of the synthetic elements of a designed connectron can be achieved in several different ways. In table 2 from one to four of the sequence elements of a connectron can be substituted by a synthetic sequence element. There are three
15 different ways of creating a synthetic sequence element. An existing sequence element somewhere in the genome can be copied into a new location. An existing sequence element can be extracted from one location in the genome and placed in another position in the genome. A new pair of sequence elements not
20 otherwise present in the genome can be created. One instance of this new, unique sequence element must be a C1 or a C2. If the first instance is a C1 then the second instance of this new, unique sequence element must be a T1. Similarly, if the first instance is a C2 then the second instance of this new, unique
25 sequence element must be a T2. Table 6 shows that there are only two ways of generating a synthetic connectron when only one synthetic sequence element is used. Implementing a new, unique sequence element is not possible because these sequence elements must come in pairs. Table 7 shows that there are 14 ways of
30 implementing a pair of synthetic sequence elements to form a synthetic connectron. Table 8 shows that there are 41 ways of implementing three synthetic sequence elements to form a

synthetic connectron. Table 9 shows that there are 25 ways of implementing four synthetic sequence elements to form a synthetic connectron.

Examples

Tables 1 thru 9 provide a large combinatorial number of ways of deleting connectrons from a genome and of adding connectrons to a genome. We give one example of deleting one connectron from a single genome and five examples of a connectron to four different genomes. It is clear that many other variations would be obvious to someone skilled in the art.

10 Deletion of a Transient Connectron from one chromosome to itself

Connectron 13 is an example of a transient connectron in the *S. cerevisiae* genome. As per table 1, this connectron can be deleted by either deleting or modifying any one or all four of the connectron elements. The C1 and the C2 identifiers are 36 while the T1 identifier is 39 and the T2 identifier is 111. When this connectron is deleted, all the properties stated below disappear.

20 The original connectron 13 is described as

Global_Id	Chromosome	C1/C2		Chromosome	T1-T2		Connectron_Type
		C1_Id	C2_Id		T1_Id	T2_Id	
13	1	36	36	1	39	111	transient

25

The C1/C2 source of the transient connectron 13 is represented in table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
CPT	36	1	1	12.572	12.788	.217	OS->

30

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 13 as shown in table 1 is represented as

	Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
15	TP	39	1	1	12.572	12.807	.236	*-----*
	TN	40	8	1	12.908	12.964	.057	*-----*
	CNT	41	1	1	12.908	12.964	.057	-->
	CPT	42	1	1	12.908	12.964	.057	-->
20	TP	43	1	1	12.922	12.964	.043	*-----*
	CNT	44	1	1	12.966	12.986	.021	-->
	CPT	45	8	1	12.966	12.986	.021	-->
	TP	46	1	1	12.966	12.986	.021	*-----*
	TN	47	1	1	13.027	13.159	.133	*-----*
25	CNT	48	1	1	13.028	13.099	.072	OS->
	TP	49	1	1	13.028	13.099	.072	*-----*
	CPT	50	1	1	13.053	13.124	.072	OS->
	TP	51	1	1	13.102	13.159	.058	*-----*
	CNT	52	1	1	13.105	13.246	.142	-->
30	CPT	53	1	1	13.130	13.246	.117	-->
	TN	54	1	1	13.176	13.194	.019	*-----*
	TN	55	1	1	13.196	13.231	.036	*-----*
	TP	56	1	1	13.211	13.246	.036	*-----*
	CPT	57	1	1	13.253	13.290	.038	-->
35	TN	58	1	1	13.253	13.290	.038	*-----*
	TP	59	1	1	13.255	13.285	.031	*-----*
	CNT	60	1	1	13.255	13.290	.036	-->
	CPT	61	8	1	13.295	13.315	.021	-->
	TN	62	8	1	13.295	13.317	.023	*-----*
40	CNT	63	8	1	13.340	13.379	.040	-->
	CPT	64	8	1	13.341	13.380	.040	-->

	GG	65	1	1	13.364	13.744	.381	Group0004	
	CPT	66	1	1	13.387	13.405	.019	-->	
	TN	67	8	1	13.387	13.413	.027		*-+++++
	TP	68	1	1	13.444	13.460	.017		*-+++++
5	CPT	69	8	1	13.566	13.582	.017	-->	
	TN	70	8	1	13.574	13.591	.018		*-+++++
	CPT	71	8	1	13.585	13.599	.016	-->	
	TN	72	1	1	13.656	13.681	.026		*-+++++
	TP	73	1	1	13.656	13.706	.051		*-+++++
10	TN	74	9	1	13.704	13.726	.023		*-+++++
	CPT	75	1	1	13.709	13.726	.018	-->	
	TN	76	1	1	13.734	13.750	.017		*-+++++
	CPT	77	1	1	13.734	13.782	.049	-->	
	TP	78	1	1	13.734	13.782	.049		*-+++++
15	TN	79	1	1	13.768	13.782	.015		*-+++++
	CPT	80	1	1	13.815	13.858	.044	-->	
	TN	81	1	1	13.840	13.858	.019		*-+++++
	CPT	82	1	1	14.422	14.460	.039	-->	
	CPT	83	1	1	14.941	14.962	.022	-->	
20	CPT	84	1	1	14.966	14.993	.028	-->	
	CPT	85	1	1	14.997	15.018	.022	-->	
	TP	86	1	1	15.795	15.816	.022		*-+++++
	TP	87	1	1	15.996	16.020	.025		*-++*
	TP	88	1	1	16.874	16.898	.025		*-++-+
25	CNT	89	1	1	20.136	20.151	.016	-->	
	CNT	90	1	1	20.157	20.176	.020	-->	
	GG	91	1	1	21.526	21.852	.327	Group0005	
	CPT	92	1	1	22.257	22.304	.048	-->	
	CNT	93	1	1	22.275	22.304	.030	-->	
30	CNT	94	1	1	22.307	22.322	.016	-->	
	CPT	95	1	1	22.307	22.322	.016	-->	
	CNT	96	1	1	22.324	22.338	.015	-->	
	CNT	97	1	1	22.351	22.367	.017	-->	
	CPT	98	8	1	22.351	22.367	.017	-->	
35	CNT	99	1	1	22.376	22.392	.017	-->	
	CPT	100	8	1	22.376	22.392	.017	-->	
	TN	101	1	1	23.300	23.324	.025		*-++*
	CPT	102	8	1	23.683	23.716	.034	-->	
	GG	103	1	1	24.001	27.969	3.969	Group0006	
40	TN	104	1	1	24.119	24.431	.313		*-++++*
	CPT	105	1	1	24.283	24.352	.070	OS->	
	TP	106	1	1	24.287	24.431	.145		*-++++-+*
	TN	107	1	1	24.433	24.514	.082		*-++++-*
	TN	108	1	1	24.516	24.603	.088		*-++++-----*
45	TN	109	8	1	24.605	24.703	.099		*-++++-----*
	TN	110	1	1	24.743	24.854	.112		*-++++-----*
	TP	111	1	1	24.863	25.001	.039		*-++++-----+***+*

The "Type" descriptor of the T1 (Id number 39) is "TP" showing that is T1 target is on the positive strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 111) also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Group0004 (Id number 65) has the type descriptor "GG". The same is true for Group0006 (Id number 103).

Group0004 through Group0006 are described in table 2 as

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YAL064C-A	-	1	negative	13.364	13.744	.381

Group0005

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
YAL064W	-	1	positive	21.526	21.852	.327

Group0006

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
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FL09	-	1 negative	24.001	27.969	3.969
------	---	------------	--------	--------	-------

All of the data for the transient connectron 13 are pulled together in the following table that is the "terse" description of the connectron.

```
Connectron Relationships - Global_Id  Type
                                13  transient
```

Control Sequences - Direction	Chromosome	C1/C2_Id	Start	Stop	Length
positive	1	36	12.572	12.788	.217

Trigger Gene - Name	COG_Id	Start	Stop	Length
YAL064W-B	-	12.047	12.427	.381

Target Sequences	- Direction	Chromosome	Tl_Id	Start	Stop	Length
	positive	1	39	12.572	12.807	.236

T2_Id	Start	Stop	Length
111	24.863	25.001	.020

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0004	YAL064C-A	-	positive	13.364	13.744	.381
2	1	Group0005	YAL064W	-	positive	21.526	21.852	.327
3	1	Group0006	FLO9	-	positive	24.001	27.969	3.969

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	41	negative	12.964	12.908	.057
2	1	42	positive	12.908	12.964	.057
3	1	44	negative	12.986	12.966	.021
4	1	45	positive	12.966	12.986	.021
5	1	48	negative	13.099	13.028	.072
6	1	50	positive	13.053	13.124	.072
7	1	52	negative	13.246	13.105	.142
8	1	53	positive	13.130	13.246	.117
9	1	57	positive	13.253	13.290	.038
10	1	60	negative	13.290	13.255	.036
11	1	61	positive	13.295	13.315	.021
12	1	63	negative	13.379	13.340	.040
13	1	64	positive	13.341	13.380	.040
14	1	66	positive	13.387	13.405	.019
15	1	69	positive	13.566	13.582	.017

	16	1	71	positive	13.585	13.599	.016
	17	1	75	positive	13.709	13.726	.018
	18	1	77	positive	13.734	13.782	.049
5	19	1	80	positive	13.815	13.858	.044
	20	1	82	positive	14.422	14.460	.039
	21	1	83	positive	14.941	14.962	.022
	22	1	84	positive	14.966	14.993	.028
	23	1	85	positive	14.997	15.018	.022
10	24	1	89	negative	20.151	20.136	.016
	25	1	90	negative	20.176	20.157	.020
	26	1	92	positive	22.257	22.304	.048
	27	1	93	negative	22.304	22.275	.030
	28	1	94	negative	22.322	22.307	.016
15	29	1	95	positive	22.307	22.322	.016
	30	1	96	negative	22.338	22.324	.015
	31	1	97	negative	22.367	22.351	.017
	32	1	98	positive	22.351	22.367	.017
	33	1	99	negative	22.392	22.376	.017
20	34	1	100	positive	22.376	22.392	.017
	35	1	102	positive	23.683	23.716	.034
	36	1	105	positive	24.283	24.352	.070

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The verbose description of the transient connectron 13 is:

In the *Saccharomyces cerevisiae* complete genome the transient connectron number 13 is generated by the control sequence
 30 (C1/C2) whose identifier number is 36. This control sequence is on the positive strand of the genomic DNA of chromosome 1. The genomic start and stop positions of this control sequence are 12.572 KB and 12.788 KB with a length of 0.217 KB. Expression of the RNA for this connectron is triggered by the promotion of the
 35 gene whose name is YAL064W-B. The genomic start and stop positions of this gene are 12.047 KB and 12.427 KB and with a length of 0.381 KB. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the positive strand of the genomic DNA on chromosome 1. The identifier number
 40 of the initiating target sequence (T1) is 39. The genomic start

and stop positions of this initiating target sequence are 12.572 KB and 12.807 KB with a length of 0.236 KB. The identifier number of the terminating target sequence (T2) is 111. The genomic start and stop positions of this terminating target sequence are 24.863 KB and 25.001 KB with a length of 0.020 KB.

This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name YAL064C-A. The genomic start and stop positions of this gene are 13.364 KB and 13.744 KB with a length of 0.381 KB. (2) The gene that has the name YAL064W. The genomic start and stop positions of this gene are 21.526 KB and 21.852 KB with a length of 0.327 KB. (3) The gene that has the name FLO9. The genomic start and stop positions of this gene are 24.001 KB and 27.969 KB with a length of 3.969 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 41 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 12.964 KB and 12.908 KB with a length of 0.057 KB. (2) The connectron that has the identifier 42 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 12.908 KB and 12.964 KB with a length of 0.057 KB. (3) The connectron that has the identifier 44 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 12.986 KB and 12.966 KB with a length of 0.021 KB. (4) The connectron that has the identifier 45 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 12.966 KB and 12.986 KB with a length of 0.021 KB. (5) The connectron that has the identifier 48 is on chromosome 1 in the negative

direction. The genomic start and stop positions of this connectron are 13.099 KB and 13.028 KB with a length of 0.072 KB. (6) The connectron that has the identifier 50 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.053 KB and 13.124 KB with a length of 0.072 KB. (7) The connectron that has the identifier 52 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 13.246 KB and 13.105 KB with a length of 0.142 KB. (8) The connectron that has the identifier 53 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.130 KB and 13.246 KB with a length of 0.117 KB. (9) The connectron that has the identifier 57 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.253 KB and 13.290 KB with a length of 0.038 KB. (10) The connectron that has the identifier 60 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 13.290 KB and 13.255 KB with a length of 0.036 KB. (11) The connectron that has the identifier 61 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.295 KB and 13.315 KB with a length of 0.021 KB. (12) The connectron that has the identifier 63 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 13.379 KB and 13.340 KB with a length of 0.040 KB. (13) The connectron that has the identifier 64 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.341 KB and 13.380 KB with a length of 0.040 KB. (14) The connectron that has the identifier 66 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.387 KB and 13.405 KB with a length of 0.019

KB. (15) The connectron that has the identifier 69 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.566 KB and 13.582 KB with a length of 0.017 KB. (16) The connectron that has the identifier 71 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.585 KB and 13.599 KB with a length of 0.016 KB. (17) The connectron that has the identifier 75 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.709 KB and 13.726 KB with a length of 0.018 KB. (18) The connectron that has the identifier 77 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.734 KB and 13.782 KB with a length of 0.049 KB. (19) The connectron that has the identifier 80 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 13.815 KB and 13.858 KB with a length of 0.044 KB. (20) The connectron that has the identifier 82 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 14.422 KB and 14.460 KB with a length of 0.039 KB. (21) The connectron that has the identifier 83 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 14.941 KB and 14.962 KB with a length of 0.022 KB. (22) The connectron that has the identifier 84 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 14.966 KB and 14.993 KB with a length of 0.028 KB. (23) The connectron that has the identifier 85 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 14.997 KB and 15.018 KB with a length of 0.022 KB. (24) The connectron that has the identifier 89 is on chromosome 1 in the negative direction. The genomic start and

stop positions of this connectron are 20.151 KB and 20.136 KB with a length of 0.016 KB. (25) The connectron that has the identifier 90 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 20.176 KB and 20.157 KB with a length of 0.020 KB. (26) The connectron that has the identifier 92 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 22.257 KB and 22.304 KB with a length of 0.048 KB. (27) The connectron that has the identifier 93 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.304 KB and 22.275 KB with a length of 0.030 KB. (28) The connectron that has the identifier 94 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.322 KB and 22.307 KB with a length of 0.016 KB. (29) The connectron that has the identifier 95 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 22.307 KB and 22.322 KB with a length of 0.016 KB. (30) The connectron that has the identifier 96 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.338 KB and 22.324 KB with a length of 0.015 KB. (31) The connectron that has the identifier 97 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.367 KB and 22.351 KB with a length of 0.017 KB. (32) The connectron that has the identifier 98 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 22.351 KB and 22.367 KB with a length of 0.017 KB. (33) The connectron that has the identifier 99 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 22.392 KB and 22.376 KB with a length of 0.017 KB. (34) The connectron that has the

identifier 100 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 22.376 KB and 22.392 KB with a length of 0.017 KB. (35) The connectron that has the identifier 102 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 23.683 KB and 23.716 KB with a length of 0.034 KB. (36) The connectron that has the identifier 105 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 24.283 KB and 24.352 KB with a length of 0.070 KB.

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Addition of a Synthetic Connectron of Type 2 from Table 2

A synthetic connectron of type 2 in which the C1 and C2 are synthetic elements, the T1 is a synthetic element and the T2 is a natural element can be introduced into the *E. coli* genome by modifying the DNA double-strand sequences at 4626.130kb through 4626.166kb for a length of 0.036kb and by modifying the DNA double-strand sequence at 705.150kb through 705.203kb for a length of 0.054kb.

Connectron 62521 is an example of a synthetic transient connectron. It is described as

30

		C1/C2		T1-T2			
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
62521	1	4651a	4651a	1	811a	975	transient

The C1/C2 source of the transient connectron 62521 is represented in Table 1 as

5	Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
	CPT	4651a	1	1	4626.130	4626.166	.037		

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 62521 as shown in Table 1 is represented as

20	Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
	TN	811a	1	1	705.150	705.203	.054		*--
	TP	812	1	1	705.122	705.141	.020		*--
	GG	813	1	1	705.316	706.980	1.665	Group0150	
25	TN	814	1	1	707.013	707.028	.016		*--
	TP	815	1	1	707.014	707.028	.015		*--
	CPT	816	1	1	707.055	707.109	.055		-->
	TN	817	1	1	707.055	707.109	.055		*--
	TP	818	1	1	707.055	707.109	.055		*--
30	CPT	819	1	1	707.112	707.162	.051	OS->	
	TN	820	1	1	707.112	707.162	.051		*--
	TP	821	1	1	707.112	707.162	.051		*--
	GG	822	1	1	707.557	710.688	3.131	Group0151	
	CNT	823	1	1	710.633	710.647	.015	OS->	
35	TN	824	1	1	710.633	710.647	.015		*--
	CNT	825	1	1	710.652	710.666	.015		-->
	GG	826	1	1	710.828	712.755	1.927	Group0152	
	TN	827	1	1	712.281	712.296	.016		*--
	GG	828	1	1	712.781	714.421	1.641	Group0153	

	TN	829	1	1	714.481	714.518	.038	*--+
	CPT	830	1	1	714.481	714.519	.039	OS->
	TP	831	1	1	714.482	714.519	.038	*--+
5	CPT	832	1	1	714.524	714.540	.017	-->
	TN	833	1	1	714.524	714.540	.017	*--+
	TP	834	1	1	714.524	714.540	.017	*--+
	CNT	835	1	1	714.543	714.593	.051	OS->
	TN	836	1	1	714.543	714.593	.051	*--+
	TP	837	1	1	714.543	714.593	.051	*--+
10	CPT	838	1	1	714.544	714.606	.063	OS->
	GG	839	1	1	714.635	715.928	1.293	Group0154
	GN	840	1	1	715.170	715.532	.363	ybfq
	TN	841	1	1	716.085	716.103	.019	*--+
	TP	842	1	1	716.085	716.103	.019	*--+
15	GG	843	1	1	716.169	724.202	8.033	Group0155
	CNT	844	1	1	720.278	720.296	.019	-->
	GN	845	1	1	720.279	724.202	3.924	kdpe
	TP	846	1	1	721.769	721.783	.015	*--+
	TN	847	1	1	721.812	721.827	.016	*--+
20	GG	848	1	1	724.211	727.955	3.744	Group0156
	TP	849	1	1	726.665	726.679	.015	*--+
	GG	850	1	1	728.357	733.325	4.968	Group0157
	GP	851	1	1	728.806	733.325	4.520	rhsc
	CPT	852	1	1	729.408	729.446	.039	-->
25	TP	853	1	1	730.270	730.284	.015	*--+
	CPT	854	1	1	730.443	730.457	.015	-->
	CPT	855	1	1	730.468	730.482	.015	-->
	CPT	856	1	1	730.484	730.507	.024	-->
	CPT	857	1	1	731.251	731.290	.040	-->
30	TP	858	1	1	731.475	731.508	.034	*--+
	TP	859	1	1	731.512	731.562	.051	*--+
	TP	860	1	1	731.564	731.693	.130	*--+
	TP	861	1	1	731.698	731.755	.058	*--+
	TP	862	1	1	731.757	731.819	.063	*--+
35	TP	863	1	1	731.821	731.903	.083	*--+
	TP	864	1	1	731.906	732.033	.128	*--+
	CPT	865	1	1	731.994	732.016	.023	-->
	CPT	866	1	1	732.019	732.034	.016	-->
	TP	867	1	1	732.035	732.050	.016	*--+
40	TP	868	1	1	732.052	732.179	.128	*--+
	CPT	869	1	1	732.065	732.179	.115	OS->
	CPT	870	1	1	732.198	732.212	.015	-->
	TP	871	1	1	732.198	732.212	.015	*-
	CPT	872	1	1	732.214	732.233	.020	-->
45	TP	873	1	1	732.214	732.233	.020	*--+
	CPT	874	1	1	732.235	732.283	.049	-->
	TP	875	1	1	732.235	732.283	.049	*--+
	CPT	876	1	1	732.306	732.326	.021	-->

	TP	877	1	1	732.306	732.326	.021	*--+
	CPT	878	1	1	732.328	732.452	.125	-->
	TP	879	1	1	732.328	732.482	.155	*--+
	CPT	880	1	1	732.454	732.482	.029	-->
5	CPT	881	1	1	732.488	732.519	.032	-->
	TN	882	1	1	733.330	733.344	.015	*--+
	TP	883	1	1	733.330	733.344	.015	*--+
	TP	884	1	1	733.371	733.513	.143	*--+
	GG	885	1	1	733.443	735.442	2.000	Group0158
10	TP	886	1	1	733.515	733.564	.050	*--+
	TP	887	1	1	733.569	733.626	.058	*--+
	TP	888	1	1	733.628	733.645	.018	*--+
	TP	889	1	1	733.647	733.696	.050	*--+
	TP	890	1	1	733.698	733.774	.077	*--+
15	TP	891	1	1	733.776	733.904	.129	*--+
	CPT	892	1	1	733.865	733.887	.023	OS->
	CPT	893	1	1	733.890	733.905	.016	-->
	TP	894	1	1	733.906	734.050	.145	*--+
	CPT	895	1	1	733.936	734.050	.115	-->
20	TP	896	1	1	734.052	734.075	.024	*--+
	CPT	897	1	1	734.052	734.139	.088	-->
	TP	898	1	1	734.084	734.139	.056	*--+
	TP	899	1	1	734.149	734.179	.031	*--+
	CPT	900	1	1	734.164	734.321	.158	-->
25	TP	901	1	1	734.192	734.321	.130	*--+
	TP	902	1	1	734.323	734.378	.056	*--+
	CPT	903	1	1	734.323	734.381	.059	-->
	CPT	904	1	1	735.525	735.569	.045	-->
	TP	905	1	1	735.525	735.569	.045	*--+
30	CPT	906	1	1	735.606	735.703	.098	-->
	TP	907	1	1	735.606	735.703	.098	*--+
	TP	908	1	1	735.707	735.721	.015	*--+
	CPT	909	1	1	735.707	735.728	.022	-->
	TP	910	1	1	735.749	735.803	.055	*--+
35	CPT	911	1	1	735.807	735.964	.158	OS->
	TP	912	1	1	735.814	735.895	.082	*--+
	TP	913	1	1	735.905	735.934	.030	*--+
	TP	914	1	1	735.938	736.083	.146	*--+
	CPT	915	1	1	735.986	736.083	.098	OS->
40	TP	916	1	1	736.152	736.173	.022	*--+
	TP	917	1	1	736.187	736.217	.031	*--+
	TP	918	1	1	736.219	736.265	.047	*--+
	TP	919	1	1	736.288	736.334	.047	*--+
	GG	920	1	1	736.327	737.184	.858	Group0159
45	TP	921	1	1	736.349	736.469	.121	*--+
	TP	922	1	1	736.516	736.628	.113	*--+
	TP	923	1	1	736.630	736.645	.016	*--+
	TP	924	1	1	736.654	736.792	.139	*--+

	TN	925	1	1	736.654	736.809	.156	*-+
	TN	926	1	1	736.816	736.832	.017	*-+
	CPT	927	1	1	737.017	737.032	.016	-->
	CPT	928	1	1	737.035	737.057	.023	-->
5	TN	929	1	1	737.168	737.188	.021	*-++
	TP	930	1	1	737.196	737.290	.095	*-+
	CPT	931	1	1	737.261	737.275	.015	-->
	CPT	932	1	1	737.278	737.292	.015	-->
	TP	933	1	1	737.292	737.393	.102	*-+
10	GG	934	1	1	737.315	738.076	.762	Group0160
	TP	935	1	1	737.411	737.475	.065	*-+
	TP	936	1	1	737.479	737.557	.079	*-+
	TP	937	1	1	737.580	737.597	.018	*-+
	TP	938	1	1	737.605	737.626	.022	*-+
15	TP	939	1	1	737.633	737.648	.016	*-+
	TP	940	1	1	737.653	737.679	.027	*-+
	TP	941	1	1	737.683	737.752	.070	*-+
	TP	942	1	1	737.798	737.822	.025	*-+
	TP	943	1	1	737.828	737.895	.068	*-+
20	TP	944	1	1	737.897	737.931	.035	*-+
	CPT	945	1	1	737.930	737.967	.038	-->
	TP	946	1	1	737.936	737.967	.032	*-+
	TP	947	1	1	737.970	737.988	.019	*-+
	TN	948	1	1	737.990	738.015	.026	*-+
25	TP	949	1	1	737.990	738.015	.026	*-+
	TN	950	1	1	738.019	738.051	.033	*-+
	TP	951	1	1	738.019	738.051	.033	*-++
	TP	952	1	1	738.053	738.074	.022	*-+
	TN	953	1	1	738.058	738.074	.017	*-+
30	TN	954	1	1	738.107	738.126	.020	*-+
	GG	955	1	1	738.224	740.148	1.925	Group0161
	TN	956	1	1	740.172	740.213	.042	*-+
	CNT	957	1	1	740.172	740.290	.119	OS->
	CPT	958	1	1	740.172	740.290	.119	OS->
35	TP	959	1	1	740.173	740.213	.041	*-+
	TP	960	1	1	740.216	740.241	.026	*-+
	TN	961	1	1	740.216	740.288	.073	*-+
	TP	962	1	1	740.244	740.288	.045	*-+
	GG	963	1	1	740.298	757.628	17.330	Group0162
40	GP	964	1	1	742.816	745.122	2.307	ybgj
	CPT	965	1	1	744.643	744.657	.015	-->
	CPT	966	1	1	744.664	744.678	.015	-->
	GP	967	1	1	754.400	756.896	2.497	sdhc
	CPT	968	1	1	755.680	755.714	.035	-->
45	GP	969	1	1	756.912	757.628	.717	sdhb
	TN	970	1	1	757.626	757.712	.087	*-+
	CPT	971	1	1	757.628	757.712	.085	OS->
	TP	972	1	1	757.629	757.712	.084	*-+

GG	973	1	1	757.687	760.730	3.044	Group0163	
CPT	974	1	1	757.717	757.736	.020	-->	
TN	975	1	1	757.718	757.753	.036		*--*

5 The "Type" descriptor of the T1 (Id number 811a) is "TN" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 975) also has the type descriptor "TN".

10

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines

15 (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

20

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

25

Group0150 through Group0163 are described in Table 2 as

Group0150

30

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
glns	COG0008	b	1 positive	705.316	706.980	1.665

Group0151

35

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
ybfm	-	b	1 positive	707.557	708.963	1.407
ybfm	-	b	1 positive	709.013	709.339	.327
fur	COG0735	b	1 negative	709.423	709.869	.447

flda	COG0716	b	1	negative	710.158	710.688	.531
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Group0152

5	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	ybf e	-	b	1 negative	710.828	711.190	.363
	ybff	COG0596	b	1 negative	711.261	712.025	.765
	seqa	COG3057	b	1 positive	712.210	712.755	.546

10 Group0153

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
pgm	COG0033	b	1 positive	712.781	714.421	1.641

15 Group0154

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
ybf p	-	b	1 positive	714.635	715.129	.495
ybf g	-	b	1 negative	715.170	715.532	.363
20 ybf h	-	b	1 negative	715.611	715.928	.318

Group0155

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
25 pote	COG0531	b	1 negative	716.169	719.683	3.515
kdpe	COG0745	b	1 negative	720.279	724.202	3.924

Group0156

30 Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
kdpb	COG2216	b	1 negative	724.211	726.259	2.049
kdpa	COG2060	b	1 negative	726.282	727.955	1.674

Group0157

35 Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
ybf a	-	b	1 positive	728.357	728.563	.207
rhsc	-	b	1 positive	728.806	733.325	4.520

40 Group0158

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
b0703	COG3209	b	1 positive	733.443	735.442	2.000

45 Group0159

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
ybf l	-	b	1 positive	736.327	737.184	.858

Group0160

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
5	ybfd	-	b	1 positive	737.315	738.076	.762

Group0161

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
10	ybga	COG3272	b	1 positive	738.224	740.148	1.925

Group0162

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
15	ybgh	COG3104	b	1 negative	740.298	741.779	1.482
	ybgi	COG0327	b	1 positive	742.050	742.793	.744
	ybgj	COG2049	b	1 positive	742.816	745.122	2.307
	nei	COG0266	b	1 positive	745.158	745.949	.792
	abrb	-	b	1 negative	745.946	747.037	1.092
20	ybgo	-	b	1 negative	747.144	748.930	1.787
	ybgq	-	b	1 negative	748.945	751.401	2.457
	ybgd	-	b	1 negative	751.452	752.018	.567
	glta	COG0372	b	1 negative	752.408	753.691	1.284
	sdhc	COG2009	b	1 positive	754.400	756.896	2.497
25	sdhb	COG0479	b	1 positive	756.912	757.628	.717

Group0163

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
30	b0725	-	b	1 positive	757.687	760.730	3.044

All of the data for the transient connectron 62521 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id	Type
62521	transient

Control Sequences - Direction	Chromosome	C1/C2_Id	Start	Stop	Length
positive	1	4651a	4626.130	4626.166	.036

Trigger Gene - Name	COG_Id	Start	Stop	Length
sms		4623.481	4626.116	2.636

Target Sequences	- Direction	Chromosome	T1_Id	Start	Stop	Length
	negative	1	811a	705.150	705.203	.054

5

T2_Id	Start	Stop	Length
975	757.753	757.718	.036

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
10	1	Group0150	glns	COG0008	positive	705.316	706.980	1.665
	1	Group0151	ybfm	-	positive	707.557	710.688	3.131
	1	Group0151	ybfm	-	positive	709.013	709.339	.327
	1	Group0151	fur	COG0735	negative	709.869	709.423	.447
	1	Group0151	flda	COG0716	negative	710.688	710.158	.531
15	1	Group0152	ybfm	-	positive	710.828	712.755	1.927
	1	Group0152	ybff	COG0596	negative	712.025	711.261	.765
	1	Group0152	sega	COG3057	positive	712.210	712.755	.546
	1	Group0153	pgm	COG0033	positive	712.781	714.421	1.641
	1	Group0154	ybfm	-	positive	714.635	715.928	1.293
20	1	Group0154	ybfm	-	negative	715.532	715.170	.363
	1	Group0154	ybfh	-	negative	715.928	715.611	.318
	1	Group0155	pote	COG0531	positive	716.169	724.202	8.033
	1	Group0155	kdpe	COG0745	negative	724.202	720.279	3.924
	1	Group0156	kdpe	COG2216	positive	724.211	727.955	3.744
25	1	Group0156	kdpa	COG2060	negative	727.955	726.282	1.674
	1	Group0157	ybfm	-	positive	728.357	733.325	4.968
	1	Group0157	rhsc	-	positive	728.806	733.325	4.520
	1	Group0158	b0703	COG3209	positive	733.443	735.442	2.000
	1	Group0159	ybfm	-	positive	736.327	737.184	.858
30	1	Group0160	ybfd	-	positive	737.315	738.076	.762
	1	Group0161	ybgm	COG3272	positive	738.224	740.148	1.925
	1	Group0162	ybgm	COG3104	positive	740.298	757.628	17.330
	1	Group0162	ybgm	COG0327	positive	742.050	742.793	.744
	1	Group0162	ybgj	COG2049	positive	742.816	745.122	2.307
35	1	Group0162	nei	COG0266	positive	745.158	745.949	.792
	1	Group0162	abrb	-	negative	747.037	745.946	1.092
	1	Group0162	ybgm	-	negative	748.930	747.144	1.787
	1	Group0162	ybgq	-	negative	751.401	748.945	2.457
	1	Group0162	ybgd	-	negative	752.018	751.452	.567
40	1	Group0162	glta	COG0372	negative	753.691	752.408	1.284
	1	Group0162	sdhc	COG2009	positive	754.400	756.896	2.497
	1	Group0162	sdhb	COG0479	positive	756.912	757.628	.717
	1	Group0163	b0725	-	positive	757.687	760.730	3.044

45

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	816	positive	707.055	707.109	.055
2	1	819	positive	707.112	707.162	.051

5	3	1	823	negative	710.647	710.633	.015
	4	1	825	negative	710.666	710.652	.015
	5	1	830	positive	714.481	714.519	.039
	6	1	832	positive	714.524	714.540	.017
	7	1	835	negative	714.593	714.543	.051
10	8	1	838	positive	714.544	714.606	.063
	9	1	844	negative	720.296	720.278	.019
	10	1	852	positive	729.408	729.446	.039
	11	1	854	positive	730.443	730.457	.015
	12	1	855	positive	730.468	730.482	.015
15	13	1	856	positive	730.484	730.507	.024
	14	1	857	positive	731.251	731.290	.040
	15	1	865	positive	731.994	732.016	.023
	16	1	866	positive	732.019	732.034	.016
	17	1	869	positive	732.065	732.179	.115
20	18	1	870	positive	732.198	732.212	.015
	19	1	872	positive	732.214	732.233	.020
	20	1	874	positive	732.235	732.283	.049
	21	1	876	positive	732.306	732.326	.021
	22	1	878	positive	732.328	732.452	.125
25	23	1	880	positive	732.454	732.482	.029
	24	1	881	positive	732.488	732.519	.032
	25	1	892	positive	733.865	733.887	.023
	26	1	893	positive	733.890	733.905	.016
	27	1	895	positive	733.936	734.050	.115
30	28	1	897	positive	734.052	734.139	.088
	29	1	900	positive	734.164	734.321	.158
	30	1	903	positive	734.323	734.381	.059
	31	1	904	positive	735.525	735.569	.045
	32	1	906	positive	735.606	735.703	.098
35	33	1	909	positive	735.707	735.728	.022
	34	1	911	positive	735.807	735.964	.158
	35	1	915	positive	735.986	736.083	.098
	36	1	927	positive	737.017	737.032	.016
	37	1	928	positive	737.035	737.057	.023
40	38	1	931	positive	737.261	737.275	.015
	39	1	932	positive	737.278	737.292	.015
	40	1	945	positive	737.930	737.967	.038
	41	1	957	negative	740.290	740.172	.119
	42	1	958	positive	740.172	740.290	.119
45	43	1	965	positive	744.643	744.657	.015
	44	1	966	positive	744.664	744.678	.015
	45	1	968	positive	755.680	755.714	.035
	46	1	971	positive	757.628	757.712	.085
	47	1	974	positive	757.717	757.736	.020

The verbose description of the synthetic connectron 62521 is:

In the *Escherichia coli* K-12 MG1655 complete genome the transient connectron number 62521 is generated by the control sequence (C1/C2) whose identifier number is 4651a. This control sequence is on the positive strand of the genomic DNA of chromosome 1. The genomic start and stop positions of this control sequence are 4626.130 KB and 4626.166 KB with a length of 0.036 KB. Expression of the RNA for this connectron is triggered by the promotion of the gene whose name is sms. The genomic start and stop positions of this gene are 4623.481 KB and 4626.116 KB and with a length of 2.636 KB. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the negative strand of the genomic DNA on chromosome 1. The identifier number of the initiating target sequence (T1) is 811a. The genomic start and stop positions of this initiating target sequence are 705.150 KB and 705.203 KB with a length of 0.054 KB. The identifier number of the terminating target sequence (T2) is 975. The genomic start and stop positions of this terminating target sequence are 757.753 KB and 757.718 KB with a length of 0.036 KB.

This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name glns and with a COG identifier of COG0008. The genomic start and stop positions of this gene are 705.316 KB and 706.980 KB with a length of 1.665 KB. (2) The gene that has the name ybfm. The genomic start and stop positions of this gene are 707.557 KB and 710.688 KB with a length of 3.131 KB. (3) The gene that has the name ybfn. The genomic start and stop positions of this gene are 709.013 KB and 709.339 KB with a length of 0.327 KB. (4) The gene that has the name fur and with a COG identifier of COG0735.

The genomic start and stop positions of this gene are 709.869 KB and 709.423 KB with a length of 0.447 KB. (5) The gene that has the name flda and with a COG identifier of COG0716. The genomic start and stop positions of this gene are 710.688 KB and 710.158 KB with a length of 0.531 KB. (6) The gene that has the name ybfe. The genomic start and stop positions of this gene are 710.828 KB and 712.755 KB with a length of 1.927 KB. (7) The gene that has the name ybff and with a COG identifier of COG0596. The genomic start and stop positions of this gene are 712.025 KB and 711.261 KB with a length of 0.765 KB. (8) The gene that has the name seqa and with a COG identifier of COG3057. The genomic start and stop positions of this gene are 712.210 KB and 712.755 KB with a length of 0.546 KB. (9) The gene that has the name pgm and with a COG identifier of COG0033. The genomic start and stop positions of this gene are 712.781 KB and 714.421 KB with a length of 1.641 KB. (10) The gene that has the name ybfp. The genomic start and stop positions of this gene are 714.635 KB and 715.928 KB with a length of 1.293 KB. (11) The gene that has the name ybfg. The genomic start and stop positions of this gene are 715.532 KB and 715.170 KB with a length of 0.363 KB. (12) The gene that has the name ybfh. The genomic start and stop positions of this gene are 715.928 KB and 715.611 KB with a length of 0.318 KB. (13) The gene that has the name pote and with a COG identifier of COG0531. The genomic start and stop positions of this gene are 716.169 KB and 724.202 KB with a length of 8.033 KB. (14) The gene that has the name kdpe and with a COG identifier of COG0745. The genomic start and stop positions of this gene are 724.202 KB and 720.279 KB with a length of 3.924 KB. (15) The gene that has the name kdpb and with a COG identifier of COG2216. The genomic start and stop positions of this gene are 724.211 KB and 727.955 KB with a length of 3.744 KB. (16) The gene that has the name kdpa and

with a COG identifier of COG2060. The genomic start and stop positions of this gene are 727.955 KB and 726.282 KB with a length of 1.674 KB. (17) The gene that has the name ybfa. The genomic start and stop positions of this gene are 728.357 KB and 733.325 KB with a length of 4.968 KB. (18) The gene that has the name rhsc. The genomic start and stop positions of this gene are 728.806 KB and 733.325 KB with a length of 4.520 KB. (19) The gene that has the name b0703 and with a COG identifier of COG3209. The genomic start and stop positions of this gene are 733.443 KB and 735.442 KB with a length of 2.000 KB. (20) The gene that has the name ybfl. The genomic start and stop positions of this gene are 736.327 KB and 737.184 KB with a length of 0.858 KB. (21) The gene that has the name ybfd. The genomic start and stop positions of this gene are 737.315 KB and 738.076 KB with a length of 0.762 KB. (22) The gene that has the name ybga and with a COG identifier of COG3272. The genomic start and stop positions of this gene are 738.224 KB and 740.148 KB with a length of 1.925 KB. (23) The gene that has the name ybgh and with a COG identifier of COG3104. The genomic start and stop positions of this gene are 740.298 KB and 757.628 KB with a length of 17.330 KB. (24) The gene that has the name ybgi and with a COG identifier of COG0327. The genomic start and stop positions of this gene are 742.050 KB and 742.793 KB with a length of 0.744 KB. (25) The gene that has the name ybgj and with a COG identifier of COG2049. The genomic start and stop positions of this gene are 742.816 KB and 745.122 KB with a length of 2.307 KB. (26) The gene that has the name nei and with a COG identifier of COG0266. The genomic start and stop positions of this gene are 745.158 KB and 745.949 KB with a length of 0.792 KB. (27) The gene that has the name aabr. The genomic start and stop positions of this gene are 747.037 KB and 745.946 KB with a length of 1.092 KB. (28) The gene that has the

name ybgo. The genomic start and stop positions of this gene are 748.930 KB and 747.144 KB with a length of 1.787 KB. (29) The gene that has the name ybgq. The genomic start and stop positions of this gene are 751.401 KB and 748.945 KB with a length of 2.457 KB. (30) The gene that has the name ybgd. The genomic start and stop positions of this gene are 752.018 KB and 751.452 KB with a length of 0.567 KB. (31) The gene that has the name glta and with a COG identifier of COG0372. The genomic start and stop positions of this gene are 753.691 KB and 752.408 KB with a length of 1.284 KB. (32) The gene that has the name sdhc and with a COG identifier of COG2009. The genomic start and stop positions of this gene are 754.400 KB and 756.896 KB with a length of 2.497 KB. (33) The gene that has the name sdhb and with a COG identifier of COG0479. The genomic start and stop positions of this gene are 756.912 KB and 757.628 KB with a length of 0.717 KB. (34) The gene that has the name b0725. The genomic start and stop positions of this gene are 757.687 KB and 760.730 KB with a length of 3.044 KB.

20 This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 816 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 707.055 KB and 707.109 KB with a length of 0.055 KB. (2) The connectron that has the identifier 819 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 707.112 KB and 707.162 KB with a length of 0.051 KB. (3) The connectron that has the identifier 823 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 710.647 KB and 710.633 KB with a length of 0.015 KB. (4) The connectron that has the identifier 825 is on chromosome 1 in the negative direction. The

genomic start and stop positions of this connectron are 710.666 KB and 710.652 KB with a length of 0.015 KB. (5) The connectron that has the identifier 830 is on chromosome 1 in the positive direction. The genomic start and stop positions of this
5 connectron are 714.481 KB and 714.519 KB with a length of 0.039 KB. (6) The connectron that has the identifier 832 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 714.524 KB and 714.540 KB with a length of 0.017 KB. (7) The connectron that has the
10 identifier 835 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 714.593 KB and 714.543 KB with a length of 0.051 KB. (8) The connectron that has the identifier 838 is on chromosome 1 in the positive direction. The genomic start and stop positions of this
15 connectron are 714.544 KB and 714.606 KB with a length of 0.063 KB. (9) The connectron that has the identifier 844 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 720.296 KB and 720.278 KB with a length of 0.019 KB. (10) The connectron that has the
20 identifier 852 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 729.408 KB and 729.446 KB with a length of 0.039 KB. (11) The connectron that has the identifier 854 is on chromosome 1 in the positive direction. The genomic start and stop positions of this
25 connectron are 730.443 KB and 730.457 KB with a length of 0.015 KB. (12) The connectron that has the identifier 855 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 730.468 KB and 730.482 KB with a length of 0.015 KB. (13) The connectron that has the
30 identifier 856 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 730.484 KB and 730.507 KB with a length of 0.024 KB. (14) The connectron

connectron are 732.454 KB and 732.482 KB with a length of 0.029 KB. (24) The connectron that has the identifier 881 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.488 KB and 732.519 KB
5 with a length of 0.032 KB. (25) The connectron that has the identifier 892 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 733.865 KB and 733.887 KB with a length of 0.023 KB. (26) The connectron that has the identifier 893 is on chromosome 1 in the positive
10 direction. The genomic start and stop positions of this connectron are 733.890 KB and 733.905 KB with a length of 0.016 KB. (27) The connectron that has the identifier 895 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 733.936 KB and 734.050 KB
15 with a length of 0.115 KB. (28) The connectron that has the identifier 897 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.052 KB and 734.139 KB with a length of 0.088 KB. (29) The connectron that has the identifier 900 is on chromosome 1 in the positive
20 direction. The genomic start and stop positions of this connectron are 734.164 KB and 734.321 KB with a length of 0.158 KB. (30) The connectron that has the identifier 903 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.323 KB and 734.381 KB
25 with a length of 0.059 KB. (31) The connectron that has the identifier 904 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.525 KB and 735.569 KB with a length of 0.045 KB. (32) The connectron that has the identifier 906 is on chromosome 1 in the positive
30 direction. The genomic start and stop positions of this connectron are 735.606 KB and 735.703 KB with a length of 0.098 KB. (33) The connectron that has the identifier 909 is on

chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.707 KB and 735.728 KB with a length of 0.022 KB. (34) The connectron that has the identifier 911 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.807 KB and 735.964 KB with a length of 0.158 KB. (35) The connectron that has the identifier 915 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.986 KB and 736.083 KB with a length of 0.098 KB. (36) The connectron that has the identifier 927 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.017 KB and 737.032 KB with a length of 0.016 KB. (37) The connectron that has the identifier 928 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.035 KB and 737.057 KB with a length of 0.023 KB. (38) The connectron that has the identifier 931 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.261 KB and 737.275 KB with a length of 0.015 KB. (39) The connectron that has the identifier 932 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.278 KB and 737.292 KB with a length of 0.015 KB. (40) The connectron that has the identifier 945 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 737.930 KB and 737.967 KB with a length of 0.038 KB. (41) The connectron that has the identifier 957 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 740.290 KB and 740.172 KB with a length of 0.119 KB. (42) The connectron that has the identifier 958 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 740.172 KB and 740.290 KB

with a length of 0.119 KB. (43) The connectron that has the identifier 965 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 744.643 KB and 744.657 KB with a length of 0.015 KB. (44) The connectron that has the identifier 966 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 744.664 KB and 744.678 KB with a length of 0.015 KB. (45) The connectron that has the identifier 968 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 755.680 KB and 755.714 KB with a length of 0.035 KB. (46) The connectron that has the identifier 971 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 757.628 KB and 757.712 KB with a length of 0.085 KB. (47) The connectron that has the identifier 974 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 757.717 KB and 757.736 KB with a length of 0.020 KB.

20

Addition of a Synthetic Connectron of Type 4 from Table 2

25

A synthetic connectron of type 4 in which the C1 and C2 are synthetic elements and the T1 and T2 are natural elements can be introduced into the *E. coli* genome by modifying the DNA double-strand sequences at 4626.130kb through 4626.166kb for a length of 0.036kb.

30

Connectron 62520 is an example of a synthetic transient connectron. It is described as

```

5      Global_Id  Chromosome  C1/C2      T1-T2
      62520      1          C1_Id  C2_Id  Chromosome  T1_Id  T2_Id  Connectron_Type
                        4651a  4651a      1      809    975    transient

```

The C1/C2 source of the transient connectron 62520 is represented in Table 1 as

10

```

Type      Num Jobno  Chr  Start      Stop      Length GeneName
CPT      4651a      1  1  4626.130  4626.166      .036      ||| || | |||| || | ||

```

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB).

25 The T1-T2 target of the transient connectron 62520 as shown in Table 1 is represented as

```

30      Type      Num Jobno  Chr  Start      Stop      Length GeneName
      TN      809      1  1  698.713  698.766      .054      *+++++*****+*****+
      GG      810      1  1  698.797  705.113      6.316 Group0149  ||||| |||| |
      TN      811      1  1  705.121  705.141      .021      *+++++*****+*****+
      TP      812      1  1  705.122  705.141      .020      *++-+++++---+*****+
      GG      813      1  1  705.316  706.980      1.665 Group0150  || ||||| ||||| |||||
      TN      814      1  1  707.013  707.028      .016      *+++++*****+*****+
35      TP      815      1  1  707.014  707.028      .015      *+++++*****+*****+
      CPT      816      1  1  707.055  707.109      .055      --> ||||| ||||| ||||| |||||
      TN      817      1  1  707.055  707.109      .055      *+++++*****+*****+

```

	TP	818	1	1	707.055	707.109	.055	*-+++++-----+-----+-----+
	CPT	819	1	1	707.112	707.162	.051	OS->
	TN	820	1	1	707.112	707.162	.051	*-+++++*****+*****+*****+
	TP	821	1	1	707.112	707.162	.051	*-++++-+++++-----+-----+-----+
5	GG	822	1	1	707.557	710.688	3.131	Group0151
	CNT	823	1	1	710.633	710.647	.015	OS->
	TN	824	1	1	710.633	710.647	.015	*-++++-*
	CNT	825	1	1	710.652	710.666	.015	-->
10	GG	826	1	1	710.828	712.755	1.927	Group0152
	TN	827	1	1	712.281	712.296	.016	*-++++-+++++-----+-----+-----+
	GG	828	1	1	712.781	714.421	1.641	Group0153
	TN	829	1	1	714.481	714.518	.038	*-+++++*****+*****+*****+
	CPT	830	1	1	714.481	714.519	.039	OS->
15	TP	831	1	1	714.482	714.519	.038	*-+++++-----+-----+-----+
	CPT	832	1	1	714.524	714.540	.017	-->
	TN	833	1	1	714.524	714.540	.017	*-+++++*****+*****+*****+
	TP	834	1	1	714.524	714.540	.017	*-+++++-----+-----+-----+
	CNT	835	1	1	714.543	714.593	.051	OS->
20	TN	836	1	1	714.543	714.593	.051	*-++*****+*****+*****+
	TP	837	1	1	714.543	714.593	.051	*-++-+++++-----+-----+-----+
	CPT	838	1	1	714.544	714.606	.063	OS->
	GG	839	1	1	714.635	715.928	1.293	Group0154
	GN	840	1	1	715.170	715.532	.363	ybfq
25	TN	841	1	1	716.085	716.103	.019	*-++*****+
	TP	842	1	1	716.085	716.103	.019	*-+++++-----+-----+-----+
	GG	843	1	1	716.169	724.202	8.033	Group0155
	CNT	844	1	1	720.278	720.296	.019	-->
	GN	845	1	1	720.279	724.202	3.924	kdpe
30	TP	846	1	1	721.769	721.783	.015	*-+++++-----+-----+-----+
	TN	847	1	1	721.812	721.827	.016	*-+++++-----+-----+-----+
	GG	848	1	1	724.211	727.955	3.744	Group0156
	TP	849	1	1	726.665	726.679	.015	*-+++++-----+-----+-----+
	GG	850	1	1	728.357	733.325	4.968	Group0157
35	GP	851	1	1	728.806	733.325	4.520	rhsc
	CPT	852	1	1	729.408	729.446	.039	-->
	TP	853	1	1	730.270	730.284	.015	*-+++++-----+-----+-----+
	CPT	854	1	1	730.443	730.457	.015	-->
	CPT	855	1	1	730.468	730.482	.015	-->
	CPT	856	1	1	730.484	730.507	.024	-->
40	CPT	857	1	1	731.251	731.290	.040	-->
	TP	858	1	1	731.475	731.508	.034	*-+++++-----+-----+-----+
	TP	859	1	1	731.512	731.562	.051	*-+++++-----+-----+-----+
	TP	860	1	1	731.564	731.693	.130	*-+++++-----+-----+-----+
	TP	861	1	1	731.698	731.755	.058	*-+++++-----+-----+-----+
45	TP	862	1	1	731.757	731.819	.063	*-+++++-----+-----+-----+
	TP	863	1	1	731.821	731.903	.083	*-+++++-----+-----+-----+
	TP	864	1	1	731.906	732.033	.128	*-+++++-----+-----+-----+
	CPT	865	1	1	731.994	732.016	.023	-->

	TP	914	1	1	735.938	736.083	.146		*-+++++
	CPT	915	1	1	735.986	736.083	.098	OS->	
	TP	916	1	1	736.152	736.173	.022		*-+++++
	TP	917	1	1	736.187	736.217	.031		*-+++++
5	TP	918	1	1	736.219	736.265	.047		*-+++++
	TP	919	1	1	736.288	736.334	.047		*-+++++
	GG	920	1	1	736.327	737.184	.858	Group0159	
	TP	921	1	1	736.349	736.469	.121		*-+++++
	TP	922	1	1	736.516	736.628	.113		*-+++++
10	TP	923	1	1	736.630	736.645	.016		*-+++++
	TP	924	1	1	736.654	736.792	.139		*-+++++
	TN	925	1	1	736.654	736.809	.156		*-+++++
	TN	926	1	1	736.816	736.832	.017		*-+++++
	CPT	927	1	1	737.017	737.032	.016	-->	
15	CPT	928	1	1	737.035	737.057	.023	-->	
	TN	929	1	1	737.168	737.188	.021		*-+++++
	TP	930	1	1	737.196	737.290	.095		*-***+
	CPT	931	1	1	737.261	737.275	.015	-->	
	CPT	932	1	1	737.278	737.292	.015	-->	
20	TP	933	1	1	737.292	737.393	.102		*-+---+
	GG	934	1	1	737.315	738.076	.762	Group0160	
	TP	935	1	1	737.411	737.475	.065		*-+---+
	TP	936	1	1	737.479	737.557	.079		*-+---+
	TP	937	1	1	737.580	737.597	.018		*-+---+
25	TP	938	1	1	737.605	737.626	.022		*-+---+
	TP	939	1	1	737.633	737.648	.016		*-+---+
	TP	940	1	1	737.653	737.679	.027		*-+---+
	TP	941	1	1	737.683	737.752	.070		*-+---+
	TP	942	1	1	737.798	737.822	.025		*-+---+
30	TP	943	1	1	737.828	737.895	.068		*-+---+
	TP	944	1	1	737.897	737.931	.035		*-+---+
	CPT	945	1	1	737.930	737.967	.038	-->	
	TP	946	1	1	737.936	737.967	.032		*-+---+
	TP	947	1	1	737.970	737.988	.019		*-+---+
35	TN	948	1	1	737.990	738.015	.026		*-+---+
	TP	949	1	1	737.990	738.015	.026		*-+---+
	TN	950	1	1	738.019	738.051	.033		*-+---+
	TP	951	1	1	738.019	738.051	.033		*-+---+
	TP	952	1	1	738.053	738.074	.022		*-+---+
40	TN	953	1	1	738.058	738.074	.017		*-+---+
	TN	954	1	1	738.107	738.126	.020		*-+---+
	GG	955	1	1	738.224	740.148	1.925	Group0161	
	TN	956	1	1	740.172	740.213	.042		*-***+
	CNT	957	1	1	740.172	740.290	.119	OS->	
45	CPT	958	1	1	740.172	740.290	.119	OS->	
	TP	959	1	1	740.173	740.213	.041		*-+++++
	TP	960	1	1	740.216	740.241	.026		*-+++++
	TN	961	1	1	740.216	740.288	.073		*-+++++

	TP	962	1	1	740.244	740.288	.045		*-++-+++++---+*****
	GG	963	1	1	740.298	757.628	17.330	Group0162	
	GP	964	1	1	742.816	745.122	2.307	ybgj	
5	CPT	965	1	1	744.643	744.657	.015	-->	
	CPT	966	1	1	744.664	744.678	.015	-->	
	GP	967	1	1	754.400	756.896	2.497	sdhc	
	CPT	968	1	1	755.680	755.714	.035	-->	
	GP	969	1	1	756.912	757.628	.717	sdhb	
	TN	970	1	1	757.626	757.712	.087		*-+*****+*****+*****
10	CPT	971	1	1	757.628	757.712	.085	OS->	
	TP	972	1	1	757.629	757.712	.084		*-+*****+*****+*****
	GG	973	1	1	757.687	760.730	3.044	Group0163	
	CPT	974	1	1	757.717	757.736	.020	-->	
	TN	975	1	1	757.718	757.753	.036		*-+*****+*****+*****

15

The "Type" descriptor of the T1 (Id number 809) is "TN" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 975) also has the type descriptor "TN".

20

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

25

30

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
35 TP	xx	1	1	278.452	278.892	.441	*---*

Group0149 through Group0163 are described in Table 2 as

Group0149

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
5	nagd	COG0647	b	1 negative	698.797	699.549	.753
	nagc	COG1940	b	1 negative	699.597	700.817	1.221
	naga	COG1820	b	1 negative	700.826	701.974	1.149
	nagb	COG0363	b	1 negative	702.034	702.834	.801
	nage	COG1264	b	1 positive	703.167	705.113	1.947

10 Group0150

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	glns	COG0008	b	1 positive	705.316	706.980	1.665

15 Group0151

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	ybfm	-	b	1 positive	707.557	708.963	1.407
	ybfm	-	b	1 positive	709.013	709.339	.327
20	fur	COG0735	b	1 negative	709.423	709.869	.447
	flda	COG0716	b	1 negative	710.158	710.688	.531

Group0152

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
25	ybfm	-	b	1 negative	710.828	711.190	.363
	ybff	COG0596	b	1 negative	711.261	712.025	.765
	sega	COG3057	b	1 positive	712.210	712.755	.546

30 Group0153

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	pgm	COG0033	b	1 positive	712.781	714.421	1.641

35 Group0154

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	ybfm	-	b	1 positive	714.635	715.129	.495
	ybfm	-	b	1 negative	715.170	715.532	.363
40	ybfh	-	b	1 negative	715.611	715.928	.318

Group0155

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
45	pote	COG0531	b	1 negative	716.169	719.683	3.515
	kdpe	COG0745	b	1 negative	720.279	724.202	3.924

Group0156

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	kdpb	COG2216	b	1 negative	724.211	726.259	2.049
	kdpa	COG2060	b	1 negative	726.282	727.955	1.674
5	-----						
	Group0157						
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	ybfa	-	b	1 positive	728.357	728.563	.207
10	rhsc	-	b	1 positive	728.806	733.325	4.520

	Group0158						
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
15	b0703	COG3209	b	1 positive	733.443	735.442	2.000

	Group0159						
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
20	ybfl	-	b	1 positive	736.327	737.184	.858

	Group0160						
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
25	ybfd	-	b	1 positive	737.315	738.076	.762

	Group0161						
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
30	ybga	COG3272	b	1 positive	738.224	740.148	1.925

	Group0162						
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
35	ybgh	COG3104	b	1 negative	740.298	741.779	1.482
	ybgi	COG0327	b	1 positive	742.050	742.793	.744
	ybgj	COG2049	b	1 positive	742.816	745.122	2.307
	nei	COG0266	b	1 positive	745.158	745.949	.792
	abrb	-	b	1 negative	745.946	747.037	1.092
40	ybgo	-	b	1 negative	747.144	748.930	1.787
	ybgq	-	b	1 negative	748.945	751.401	2.457
	ybgd	-	b	1 negative	751.452	752.018	.567
	glta	COG0372	b	1 negative	752.408	753.691	1.284
	sdhc	COG2009	b	1 positive	754.400	756.896	2.497
45	sdhb	COG0479	b	1 positive	756.912	757.628	.717

	Group0163						

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
b0725	-	b	1 positive	757.687	760.730	3.044

5 All of the data for the transient connectron 62520 are pulled together in the following table that is the "terse" description of the connectron.

10

Connectron Relationships - Global_Id Type
62520 transient

15 Control Sequences - Direction Chromosome C1/C2_Id Start Stop Length
positive 1 4651a 4626.130 4626.166 .036

Trigger Gene - Name COG_Id Start Stop Length
sms 4623.481 4626.116 2.636

20 Target Sequences - Direction Chromosome T1_Id Start Stop Length
negative 1 809 698.766 698.713 .054

T2_Id Start Stop Length
975 757.753 757.718 .036

25

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0149	nagd	COG0647	positive	698.797	705.113	6.316
2	1	Group0149	nagc	COG1940	negative	700.817	699.597	1.221
30 3	1	Group0149	naga	COG1820	negative	701.974	700.826	1.149
4	1	Group0149	nagb	COG0363	negative	702.834	702.034	.801
5	1	Group0149	nage	COG1264	positive	703.167	705.113	1.947
6	1	Group0150	glns	COG0008	positive	705.316	706.980	1.665
7	1	Group0151	ybfm	-	positive	707.557	710.688	3.131
35 8	1	Group0151	ybfm	-	positive	709.013	709.339	.327
9	1	Group0151	fur	COG0735	negative	709.869	709.423	.447
10	1	Group0151	flda	COG0716	negative	710.688	710.158	.531
11	1	Group0152	ybfe	-	positive	710.828	712.755	1.927
12	1	Group0152	ybff	COG0596	negative	712.025	711.261	.765
40 13	1	Group0152	seqa	COG3057	positive	712.210	712.755	.546
14	1	Group0153	pgm	COG0033	positive	712.781	714.421	1.641
15	1	Group0154	ybfp	-	positive	714.635	715.928	1.293
16	1	Group0154	ybfq	-	negative	715.532	715.170	.363
17	1	Group0154	ybfh	-	negative	715.928	715.611	.318
45 18	1	Group0155	pote	COG0531	positive	716.169	724.202	8.033
19	1	Group0155	kdpe	COG0745	negative	724.202	720.279	3.924

5	20	1	Group0156 kdpb	COG2216	positive	724.211	727.955	3.744
	21	1	Group0156 kdpa	COG2060	negative	727.955	726.282	1.674
	22	1	Group0157 ybfa	-	positive	728.357	733.325	4.968
	23	1	Group0157 rhsc	-	positive	728.806	733.325	4.520
	24	1	Group0158 b0703	COG3209	positive	733.443	735.442	2.000
10	25	1	Group0159 ybfl	-	positive	736.327	737.184	.858
	26	1	Group0160 ybfd	-	positive	737.315	738.076	.762
	27	1	Group0161 ybga	COG3272	positive	738.224	740.148	1.925
	28	1	Group0162 ybgh	COG3104	positive	740.298	757.628	17.330
	29	1	Group0162 ybgi	COG0327	positive	742.050	742.793	.744
15	30	1	Group0162 ybgj	COG2049	positive	742.816	745.122	2.307
	31	1	Group0162 nei	COG0266	positive	745.158	745.949	.792
	32	1	Group0162 abrb	-	negative	747.037	745.946	1.092
	33	1	Group0162 ybgo	-	negative	748.930	747.144	1.787
	34	1	Group0162 ybgq	-	negative	751.401	748.945	2.457
20	35	1	Group0162 ybgd	-	negative	752.018	751.452	.567
	36	1	Group0162 glta	COG0372	negative	753.691	752.408	1.284
	37	1	Group0162 sdhc	COG2009	positive	754.400	756.896	2.497
	38	1	Group0162 sdhb	COG0479	positive	756.912	757.628	.717
	39	1	Group0163 b0725	-	positive	757.687	760.730	3.044

Controlled Connectrons

	Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
25	1	1	816	positive	707.055	707.109	.055
	2	1	819	positive	707.112	707.162	.051
	3	1	823	negative	710.647	710.633	.015
	4	1	825	negative	710.666	710.652	.015
	5	1	830	positive	714.481	714.519	.039
30	6	1	832	positive	714.524	714.540	.017
	7	1	835	negative	714.593	714.543	.051
	8	1	838	positive	714.544	714.606	.063
	9	1	844	negative	720.296	720.278	.019
	10	1	852	positive	729.408	729.446	.039
35	11	1	854	positive	730.443	730.457	.015
	12	1	855	positive	730.468	730.482	.015
	13	1	856	positive	730.484	730.507	.024
	14	1	857	positive	731.251	731.290	.040
	15	1	865	positive	731.994	732.016	.023
40	16	1	866	positive	732.019	732.034	.016
	17	1	869	positive	732.065	732.179	.115
	18	1	870	positive	732.198	732.212	.015
	19	1	872	positive	732.214	732.233	.020
	20	1	874	positive	732.235	732.283	.049
45	21	1	876	positive	732.306	732.326	.021
	22	1	878	positive	732.328	732.452	.125
	23	1	880	positive	732.454	732.482	.029
	24	1	881	positive	732.488	732.519	.032
	25	1	892	positive	733.865	733.887	.023

5	26	1	893	positive	733.890	733.905	.016
	27	1	895	positive	733.936	734.050	.115
	28	1	897	positive	734.052	734.139	.088
	29	1	900	positive	734.164	734.321	.158
	30	1	903	positive	734.323	734.381	.059
	31	1	904	positive	735.525	735.569	.045
	32	1	906	positive	735.606	735.703	.098
	33	1	909	positive	735.707	735.728	.022
10	34	1	911	positive	735.807	735.964	.158
	35	1	915	positive	735.986	736.083	.098
	36	1	927	positive	737.017	737.032	.016
	37	1	928	positive	737.035	737.057	.023
	38	1	931	positive	737.261	737.275	.015
15	39	1	932	positive	737.278	737.292	.015
	40	1	945	positive	737.930	737.967	.038
	41	1	957	negative	740.290	740.172	.119
	42	1	958	positive	740.172	740.290	.119
	43	1	965	positive	744.643	744.657	.015
	44	1	966	positive	744.664	744.678	.015
20	45	1	968	positive	755.680	755.714	.035
	46	1	971	positive	757.628	757.712	.085
	47	1	974	positive	757.717	757.736	.020

25

The verbose description of the synthetic connectron 62520 is:

In the Escherichia coli K-12 MG1655 complete genome the transient connectron number 62520 is generated by the control sequence (C1/C2) whose identifier number is 4651a. This control sequence is on the positive strand of the genomic DNA of chromosome 1. The genomic start and stop positions of this control sequence are 4626.130 KB and 4626.166 KB with a length of 0.036 KB. Expression of the RNA for this connectron is triggered by the promotion of the gene whose name is sms. The genomic start and stop positions of this gene are 4623.481 KB and 4626.116 KB and with a length of 2.636 KB. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the negative strand of the genomic DNA on chromosome 1. The identifier number of the initiating target

sequence (T1) is 809. The genomic start and stop positions of this initiating target sequence are 698.766 KB and 698.713 KB with a length of 0.054 KB. The identifier number of the terminating target sequence (T2) is 975. The genomic start and stop positions of this terminating target sequence are 757.753 KB and 757.718 KB with a length of 0.036 KB.

This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name nagd and with a COG identifier of COG0647. The genomic start and stop positions of this gene are 698.797 KB and 705.113 KB with a length of 6.316 KB. (2) The gene that has the name nagc and with a COG identifier of COG1940. The genomic start and stop positions of this gene are 700.817 KB and 699.597 KB with a length of 1.221 KB. (3) The gene that has the name naga and with a COG identifier of COG1820. The genomic start and stop positions of this gene are 701.974 KB and 700.826 KB with a length of 1.149 KB. (4) The gene that has the name nagb and with a COG identifier of COG0363. The genomic start and stop positions of this gene are 702.834 KB and 702.034 KB with a length of 0.801 KB. (5) The gene that has the name nage and with a COG identifier of COG1264. The genomic start and stop positions of this gene are 703.167 KB and 705.113 KB with a length of 1.947 KB. (6) The gene that has the name glns and with a COG identifier of COG0008. The genomic start and stop positions of this gene are 705.316 KB and 706.980 KB with a length of 1.665 KB. (7) The gene that has the name ybfm. The genomic start and stop positions of this gene are 707.557 KB and 710.688 KB with a length of 3.131 KB. (8) The gene that has the name ybfn. The genomic start and stop positions of this gene are 709.013 KB and 709.339 KB with a length of 0.327 KB. (9) The gene that has the name fur and with a COG identifier of COG0735.

The genomic start and stop positions of this gene are 709.869 KB and 709.423 KB with a length of 0.447 KB. (10) The gene that has the name flda and with a COG identifier of COG0716. The genomic start and stop positions of this gene are 710.688 KB and 710.158
5 KB with a length of 0.531 KB. (11) The gene that has the name ybfe. The genomic start and stop positions of this gene are 710.828 KB and 712.755 KB with a length of 1.927 KB. (12) The gene that has the name ybff and with a COG identifier of COG0596. The genomic start and stop positions of this gene are
10 712.025 KB and 711.261 KB with a length of 0.765 KB. (13) The gene that has the name seqa and with a COG identifier of COG3057. The genomic start and stop positions of this gene are 712.210 KB and 712.755 KB with a length of 0.546 KB. (14) The gene that has the name pgm and with a COG identifier of COG0033.
15 The genomic start and stop positions of this gene are 712.781 KB and 714.421 KB with a length of 1.641 KB. (15) The gene that has the name ybfp. The genomic start and stop positions of this gene are 714.635 KB and 715.928 KB with a length of 1.293 KB. (16) The gene that has the name ybfg. The genomic start and
20 stop positions of this gene are 715.532 KB and 715.170 KB with a length of 0.363 KB. (17) The gene that has the name ybfh. The genomic start and stop positions of this gene are 715.928 KB and 715.611 KB with a length of 0.318 KB. (18) The gene that has the name pote and with a COG identifier of COG0531. The genomic
25 start and stop positions of this gene are 716.169 KB and 724.202 KB with a length of 8.033 KB. (19) The gene that has the name kdpe and with a COG identifier of COG0745. The genomic start and stop positions of this gene are 724.202 KB and 720.279 KB with a length of 3.924 KB. (20) The gene that has the name kdpb
30 and with a COG identifier of COG2216. The genomic start and stop positions of this gene are 724.211 KB and 727.955 KB with a length of 3.744 KB. (21) The gene that has the name kdpa and

with a COG identifier of COG2060. The genomic start and stop positions of this gene are 727.955 KB and 726.282 KB with a length of 1.674 KB. (22) The gene that has the name ybfa. The genomic start and stop positions of this gene are 728.357 KB and 733.325 KB with a length of 4.968 KB. (23) The gene that has the name rhsc. The genomic start and stop positions of this gene are 728.806 KB and 733.325 KB with a length of 4.520 KB. (24) The gene that has the name b0703 and with a COG identifier of COG3209. The genomic start and stop positions of this gene are 733.443 KB and 735.442 KB with a length of 2.000 KB. (25) The gene that has the name ybfl. The genomic start and stop positions of this gene are 736.327 KB and 737.184 KB with a length of 0.858 KB. (26) The gene that has the name ybfd. The genomic start and stop positions of this gene are 737.315 KB and 738.076 KB with a length of 0.762 KB. (27) The gene that has the name ybga and with a COG identifier of COG3272. The genomic start and stop positions of this gene are 738.224 KB and 740.148 KB with a length of 1.925 KB. (28) The gene that has the name ybgh and with a COG identifier of COG3104. The genomic start and stop positions of this gene are 740.298 KB and 757.628 KB with a length of 17.330 KB. (29) The gene that has the name ybgi and with a COG identifier of COG0327. The genomic start and stop positions of this gene are 742.050 KB and 742.793 KB with a length of 0.744 KB. (30) The gene that has the name ybgj and with a COG identifier of COG2049. The genomic start and stop positions of this gene are 742.816 KB and 745.122 KB with a length of 2.307 KB. (31) The gene that has the name nei and with a COG identifier of COG0266. The genomic start and stop positions of this gene are 745.158 KB and 745.949 KB with a length of 0.792 KB. (32) The gene that has the name abrb. The genomic start and stop positions of this gene are 747.037 KB and 745.946 KB with a length of 1.092 KB. (33) The gene that has the

name ybgo. The genomic start and stop positions of this gene are 748.930 KB and 747.144 KB with a length of 1.787 KB. (34) The gene that has the name ybgq. The genomic start and stop positions of this gene are 751.401 KB and 748.945 KB with a length of 2.457 KB. (35) The gene that has the name ybgd. The genomic start and stop positions of this gene are 752.018 KB and 751.452 KB with a length of 0.567 KB. (36) The gene that has the name glta and with a COG identifier of COG0372. The genomic start and stop positions of this gene are 753.691 KB and 752.408 KB with a length of 1.284 KB. (37) The gene that has the name sdhc and with a COG identifier of COG2009. The genomic start and stop positions of this gene are 754.400 KB and 756.896 KB with a length of 2.497 KB. (38) The gene that has the name sdhb and with a COG identifier of COG0479. The genomic start and stop positions of this gene are 756.912 KB and 757.628 KB with a length of 0.717 KB. (39) The gene that has the name b0725. The genomic start and stop positions of this gene are 757.687 KB and 760.730 KB with a length of 3.044 KB.

20 This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 816 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 707.055 KB and 707.109 KB with a length of 0.055 KB. (2) The connectron that has the identifier 819 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 707.112 KB and 707.162 KB with a length of 0.051 KB. (3) The connectron that has the identifier 823 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 710.647 KB and 710.633 KB with a length of 0.015 KB. (4) The connectron that has the identifier 825 is on chromosome 1 in the negative direction. The

genomic start and stop positions of this connectron are 710.666 KB and 710.652 KB with a length of 0.015 KB. (5) The connectron that has the identifier 830 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

5 connectron are 714.481 KB and 714.519 KB with a length of 0.039 KB. (6) The connectron that has the identifier 832 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 714.524 KB and 714.540 KB with a length of 0.017 KB. (7) The connectron that has the

10 identifier 835 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 714.593 KB and 714.543 KB with a length of 0.051 KB. (8) The connectron that has the identifier 838 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

15 connectron are 714.544 KB and 714.606 KB with a length of 0.063 KB. (9) The connectron that has the identifier 844 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 720.296 KB and 720.278 KB with a length of 0.019 KB. (10) The connectron that has the

20 identifier 852 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 729.408 KB and 729.446 KB with a length of 0.039 KB. (11) The connectron that has the identifier 854 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

25 connectron are 730.443 KB and 730.457 KB with a length of 0.015 KB. (12) The connectron that has the identifier 855 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 730.468 KB and 730.482 KB with a length of 0.015 KB. (13) The connectron that has the

30 identifier 856 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 730.484 KB and 730.507 KB with a length of 0.024 KB. (14) The connectron

that has the identifier 857 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 731.251 KB and 731.290 KB with a length of 0.040 KB. (15) The connectron that has the identifier 865 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 731.994 KB and 732.016 KB with a length of 0.023 KB. (16) The connectron that has the identifier 866 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.019 KB and 732.034 KB with a length of 0.016 KB. (17) The connectron that has the identifier 869 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.019 KB and 732.065 KB with a length of 0.046 KB. (18) The connectron that has the identifier 870 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.198 KB and 732.212 KB with a length of 0.015 KB. (19) The connectron that has the identifier 872 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.214 KB and 732.233 KB with a length of 0.020 KB. (20) The connectron that has the identifier 874 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.235 KB and 732.283 KB with a length of 0.049 KB. (21) The connectron that has the identifier 876 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.306 KB and 732.326 KB with a length of 0.021 KB. (22) The connectron that has the identifier 878 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.328 KB and 732.452 KB with a length of 0.125 KB. (23) The connectron that has the identifier 880 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

connectron are 732.454 KB and 732.482 KB with a length of 0.029 KB. (24) The connectron that has the identifier 881 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 732.488 KB and 732.519 KB with a length of 0.032 KB. (25) The connectron that has the identifier 892 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 733.865 KB and 733.887 KB with a length of 0.023 KB. (26) The connectron that has the identifier 893 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 733.890 KB and 733.905 KB with a length of 0.016 KB. (27) The connectron that has the identifier 895 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 733.936 KB and 734.050 KB with a length of 0.115 KB. (28) The connectron that has the identifier 897 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.052 KB and 734.139 KB with a length of 0.088 KB. (29) The connectron that has the identifier 900 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.164 KB and 734.321 KB with a length of 0.158 KB. (30) The connectron that has the identifier 903 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.323 KB and 734.381 KB with a length of 0.059 KB. (31) The connectron that has the identifier 904 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.525 KB and 735.569 KB with a length of 0.045 KB. (32) The connectron that has the identifier 906 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 735.606 KB and 735.703 KB with a length of 0.098 KB. (33) The connectron that has the identifier 909 is on

chromosome 1 in the positive direction. The genomic start and
 stop positions of this connectron are 735.707 KB and 735.728 KB
 with a length of 0.022 KB. (34) The connectron that has the
 identifier 911 is on chromosome 1 in the positive direction. The
 5 genomic start and stop positions of this connectron are 735.807
 KB and 735.964 KB with a length of 0.158 KB. (35) The connectron
 that has the identifier 915 is on chromosome 1 in the positive
 direction. The genomic start and stop positions of this
 connectron are 735.986 KB and 736.083 KB with a length of 0.098
 10 KB. (36) The connectron that has the identifier 927 is on
 chromosome 1 in the positive direction. The genomic start and
 stop positions of this connectron are 737.017 KB and 737.032 KB
 with a length of 0.016 KB. (37) The connectron that has the
 identifier 928 is on chromosome 1 in the positive direction. The
 15 genomic start and stop positions of this connectron are 737.035
 KB and 737.057 KB with a length of 0.023 KB. (38) The connectron
 that has the identifier 931 is on chromosome 1 in the positive
 direction. The genomic start and stop positions of this
 connectron are 737.261 KB and 737.275 KB with a length of 0.015
 20 KB. (39) The connectron that has the identifier 932 is on
 chromosome 1 in the positive direction. The genomic start and
 stop positions of this connectron are 737.278 KB and 737.292 KB
 with a length of 0.015 KB. (40) The connectron that has the
 identifier 945 is on chromosome 1 in the positive direction. The
 25 genomic start and stop positions of this connectron are 737.930
 KB and 737.967 KB with a length of 0.038 KB. (41) The connectron
 that has the identifier 957 is on chromosome 1 in the negative
 direction. The genomic start and stop positions of this
 connectron are 740.290 KB and 740.172 KB with a length of 0.119
 30 KB. (42) The connectron that has the identifier 958 is on
 chromosome 1 in the positive direction. The genomic start and
 stop positions of this connectron are 740.172 KB and 740.290 KB

with a length of 0.119 KB. (43) The connectron that has the identifier 965 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 744.643 KB and 744.657 KB with a length of 0.015 KB. (44) The connectron that has the identifier 966 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 744.664 KB and 744.678 KB with a length of 0.015 KB. (45) The connectron that has the identifier 968 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 755.680 KB and 755.714 KB with a length of 0.035 KB. (46) The connectron that has the identifier 971 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 757.628 KB and 757.712 KB with a length of 0.085 KB. (47) The connectron that has the identifier 974 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 757.717 KB and 757.736 KB with a length of 0.020 KB.

Addition of a Synthetic Transient Connectron between chromosomes - Type 7 from Table 2

A synthetic virtual connectron of type 7 in which the C1 is a synthetic element and C2 is a natural element, the T1 is a natural element and the T2 is a synthetic element can be introduced into the *S. cerevisiae* genome by modifying the DNA double-strand sequence at 221.330kb through 221.345kb on chromosome 2 for a length of 0.016kb and by modifying the DNA

double-strand sequence at 488.140kb through 488.297 on chromosome 5 for a length of 0.158kb.

To create this example of a synthetic connectron of type 7 the T2 sequence for natural connectron 3558 (old position 497.581kb through 498.091kb) was copied into the new position stated above.

Connectron 75273 is an example of a transient connectron. It is described as

Global_Id	Chromosome	C1/C2		Chromosome	T1-T2		Connectron_Type
		C1_Id	C2_Id		T1_Id	T2_Id	
75273	2	792a	793	5	4749	4824a	transient

The C1/C2 source of the transient connectron 75273 is represented in table 1 as

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
CPT	792a	22	2	221.330	221.345	.016	-->
CPT	793	22	2	221.346	221.361	.016	-->

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB). The symbol OS-> occurs because there is another connectron formed by this C1/C2 that happens to be a one-shot connectron.

The T1-T2 target of the transient connectron 75273 as shown in table 1 is represented as

5	Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
	TN	4749	59	5	448.454	448.992	.539		*-*
	TP	4750	68	5	448.454	448.992	.539		*-+
	CNT	4751	64	5	448.454	448.992	.539	-->	
	TP	4752	63	5	449.003	449.315	.313		*-+
10	TN	4753	65	5	449.003	449.315	.313		*-+
	CNT	4754	60	5	449.003	449.315	.313	OS->	
	CNT	4755	5	5	449.317	449.482	.166	OS->	
	TN	4756	5	5	449.317	449.482	.166		*-+
	TP	4757	64	5	449.317	449.482	.148		*-+
15	GG	4758	59	5	449.470	449.574	.105	Group0615	
	CPT	4759	70	5	449.490	449.563	.074	-->	
	TN	4760	70	5	449.490	449.563	.074		*-+
	TP	4761	67	5	449.490	449.558	.069		*-+
	CNT	4762	70	5	449.490	449.563	.074	-->	
20	TN	4763	59	5	449.575	449.603	.029		*-+
	TP	4764	59	5	449.575	449.603	.029		*-+
	GG	4765	59	5	450.558	453.230	2.672	Group0616	
	TP	4766	59	5	452.176	452.190	.015		*-+
	GG	4767	59	5	453.454	454.914	1.461	Group0617	
25	CNT	4768	20	5	453.909	453.923	.015	-->	
	CNT	4769	20	5	453.928	453.942	.015	-->	
	TP	4770	59	5	454.644	454.658	.015		*-+
	GG	4771	59	5	455.141	457.600	2.460	Group0618	
	TN	4772	66	5	456.316	456.331	.016		*-+
30	GG	4773	59	5	457.801	460.218	2.418	Group0619	
	TN	4774	66	5	460.340	460.355	.016		*-+
	GG	4775	59	5	460.521	466.020	5.500	Group0620	
	GP	4776	59	5	462.580	462.861	.282	LSM5	
	TN	4777	59	5	463.743	463.758	.016		*-+
35	TP	4778	59	5	463.743	463.758	.016		*-+
	CPT	4779	61	5	463.990	464.004	.015	-->	
	CPT	4780	61	5	464.010	464.024	.015	-->	
	TP	4781	59	5	465.739	465.754	.016		*-
	GG	4782	59	5	466.203	468.811	2.609	Group0621	
40	GP	4783	59	5	468.365	468.811	.447	SPI1	
	TP	4784	69	5	469.451	469.518	.059		*-+
	CNT	4785	67	5	469.451	469.530	.080	OS->	
	GG	4786	59	5	469.452	469.525	.074	Group0622	
	TN	4787	59	5	469.452	469.532	.081		*-+
45	CPT	4788	67	5	469.452	469.531	.080	-->	
	GG	4789	59	5	469.681	472.419	2.739	Group0623	

	TN	4790	20	5	471.772	471.786	.015	*-+
	TP	4791	20	5	471.772	471.786	.015	*-+
	GG	4792	59	5	472.652	482.843	10.192 Group0624	
	GP	4793	59	5	475.015	476.223	1.209 OXA1	
5	TP	4794	63	5	476.803	476.817	.015	*-+
	CPT	4795	60	5	478.412	478.426	.015	-->
	CPT	4796	60	5	478.436	478.450	.015	-->
	CNT	4797	47	5	481.782	481.812	.031	-->
10	TN	4798	20	5	482.192	482.206	.015	*-+
	CNT	4799	67	5	482.676	482.690	.015	-->
	CNT	4800	67	5	482.701	482.715	.015	-->
	GG	4801	59	5	483.320	487.188	3.869 Group0625	
	GP	4802	59	5	484.783	487.188	2.406 SEC34	
	CNT	4803	61	5	485.099	485.113	.015	-->
15	CNT	4804	61	5	485.119	485.134	.016	-->
	TN	4805	64	5	487.041	487.056	.016	*-+
	GG	4806	59	5	487.326	487.397	.072 Group0626	
	CPT	4807	61	5	487.375	487.397	.023	-->
	CPT	4808	61	5	487.400	487.415	.016	-->
20	CNT	4809	34	5	487.830	487.848	.019	OS->
	CPT	4810	62	5	487.830	487.848	.019	OS->
	TP	4811	60	5	487.830	487.848	.019	*-+
	TN	4812	59	5	487.830	487.848	.019	*-+
	CNT	4813	34	5	487.850	488.016	.167	OS->
25	CPT	4814	5	5	487.850	488.016	.167	OS->
	TP	4815	5	5	487.850	488.016	.167	*-+
	TN	4816	64	5	487.850	488.016	.167	*-+
	CNT	4817	47	5	488.024	488.137	.114	OS->
	CPT	4818	47	5	488.024	488.068	.045	-->
30	TN	4819	34	5	488.024	488.067	.044	*-+
	TP	4820	34	5	488.024	488.067	.044	*-+
	CPT	4821	69	5	488.069	488.137	.069	OS->
	TN	4822	67	5	488.069	488.122	.054	*-+
	TP	4823	59	5	488.069	488.085	.017	*-+
35	TP	4824	5	5	488.094	488.137	.044	*-+
	TN	4824a	5	5	488.140	488.297	.158	*-*

The "Type" descriptor of the T1 (Id number 4749) is "TN" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 4824a) also has the type descriptor "TN".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Group0615 (Id number 4758) has the type descriptor "GG". The same is true for Group0626 (Id number 4806).

Group0615 through Group0626 are described in table 2 as

Group0615							
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
25	YER138W-A	-	5	positive	449.470	449.574	.105

Group0616							
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
30	YER139C	-	5	negative	450.558	451.238	.681
	YER140W	-	5	positive	451.560	453.230	1.671

Group0617							
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
35	COX15	COG1612	0	5 positive	453.454	454.914	1.461

Group0618							
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
40	MAG1	COG0122	L	5 negative	455.141	456.031	.891

DDI1	-	5	positive	456.314	457.600	1.287
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Group0619

5	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	UBP5	-	5	negative	457.801	460.218	2.418

Group0620

10	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	FTR1	COG0672	P	5 negative	460.521	461.735	1.215
	LSM5	COG1958	K	5 positive	462.580	462.861	.282
	YER147C	-	5	negative	462.963	464.837	1.875
	SPT15	COG2101	K	5 positive	465.298	466.020	.723

15

Group0621

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	PEA2	-	5	negative	466.203	467.465	1.263
20	SPI1	-	5	positive	468.365	468.811	.447

Group0622

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
25			5	positive	469.452	469.525	.074

Group0623

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
30	UBP3	-	5	negative	469.681	472.419	2.739

Group0624

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
35	YER152C	COG1167	K	5 negative	472.652	473.983	1.332
	PET122	-	5	negative	474.036	474.800	.765
	OXA1	COG0706	N	5 positive	475.015	476.223	1.209
	BEM2	-	5	negative	476.340	482.843	6.504

40

Group0625

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	YER156C	-	5	negative	483.320	484.336	1.017
	SEC34	-	5	positive	484.783	487.188	2.406

45

Group0626

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
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5 positive 487.326 487.397 .072

All of the data for the transient connectron 75273 are pulled together in the following table that is the "terse" description of the connectron.

10 Connectron Relationships - Global_Id Type
75273 transient

Control Sequences - Direction Chromosome C1/C2_Id Start Stop Length
positive 2 792a 221.330 221.345 .016
15 positive 2 793 221.346 221.361 .016

Trigger Gene - Name COG_Id Start Stop Length
YBL005W-B - 221.293 226.561 5.269

20 Target Sequences - Direction Chromosome T1_Id Start Stop Length
negative 5 4749 448.992 448.454 .539

T2_Id Start Stop Length
4824a 488.140 488.297 .158

25 Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	5	Group0615	YER138W-A	-	positive	449.470	449.574	.105
2	5	Group0616	YER139C	-	positive	450.558	453.230	2.673
3	5	Group0616	YER140W	-	positive	451.560	453.230	1.671
4	5	Group0617	COX15	COG1612	positive	453.454	454.914	1.461
5	5	Group0618	MAG1	COG0122	positive	455.141	457.600	2.459
6	5	Group0618	DDI1	-	positive	456.314	457.600	1.287
7	5	Group0619	UBP5	-	positive	457.801	460.218	2.418
8	5	Group0620	FTR1	COG0672	positive	460.521	466.020	5.499
9	5	Group0620	LSM5	COG1958	positive	462.580	462.861	.282
10	5	Group0620	YER147C	-	negative	464.837	462.963	1.875
11	5	Group0620	SPT15	COG2101	positive	465.298	466.020	.723
12	5	Group0621	PEA2	-	positive	466.203	468.811	2.608
13	5	Group0621	SPI1	-	positive	468.365	468.811	.447
14	5	Group0622			positive	469.452	469.525	.074
15	5	Group0623	UBP3	-	positive	469.681	472.419	2.739
16	5	Group0624	YER152C	COG1167	positive	472.652	482.843	10.191
17	5	Group0624	PET122	-	negative	474.800	474.036	.765
18	5	Group0624	OXA1	COG0706	positive	475.015	476.223	1.209
19	5	Group0624	BEM2	-	negative	482.843	476.340	6.504

20	5	Group0625 YER156C	-	positive	483.320	487.188	3.868
21	5	Group0625 SEC34	-	positive	484.783	487.188	2.406
22	5	Group0626		positive	487.326	487.397	.072

5 Controlled Connectrons

	Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
	1	5	4751	negative	448.992	448.454	.539
	2	5	4754	negative	449.315	449.003	.313
	3	5	4755	negative	449.482	449.317	.166
10	4	5	4759	positive	449.490	449.563	.074
	5	5	4762	negative	449.563	449.490	.074
	6	5	4768	negative	453.923	453.909	.015
	7	5	4769	negative	453.942	453.928	.015
	8	5	4779	positive	463.990	464.004	.015
15	9	5	4780	positive	464.010	464.024	.015
	10	5	4785	negative	469.530	469.451	.080
	11	5	4788	positive	469.452	469.531	.080
	12	5	4795	positive	478.412	478.426	.015
	13	5	4796	positive	478.436	478.450	.015
20	14	5	4797	negative	481.812	481.782	.031
	15	5	4799	negative	482.690	482.676	.015
	16	5	4800	negative	482.715	482.701	.015
	17	5	4803	negative	485.113	485.099	.015
	18	5	4804	negative	485.134	485.119	.016
25	19	5	4807	positive	487.375	487.397	.023
	20	5	4808	positive	487.400	487.415	.016
	21	5	4809	negative	487.848	487.830	.019
	22	5	4810	positive	487.830	487.848	.019
	23	5	4813	negative	488.016	487.850	.167
30	24	5	4814	positive	487.850	488.016	.167
	25	5	4817	negative	488.137	488.024	.114
	26	5	4818	positive	488.024	488.068	.045
	27	5	4821	positive	488.069	488.137	.069

35 -----

The verbose description of the transient connectron 75273 is:

40 In the *Saccharomyces cerevisiae* complete genome the transient connectron number 75273 is generated by the control sequence C1 whose identifier number is 792a. This control sequence is on the positive strand of the genomic DNA of chromosome 2. The genomic start and stop positions of this control sequence are 221.330 KB and 221.345 KB with a length of 0.016 KB and by the control

sequence C2 whose identifier number is 793. This control sequence is on the positive strand of the genomic DNA of chromosome 2. The genomic start and stop positions of this control sequence are 221.346 KB and 221.361 KB with a length of 0.016 KB. Expression of the RNA for this connectron is triggered by the promotion of the gene whose name is YBL005W-B. The genomic start and stop positions of this gene are 221.293 KB and 226.561 KB and with a length of 5.269 KB. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the negative strand of the genomic DNA on chromosome 5. The identifier number of the initiating target sequence (T1) is 4749. The genomic start and stop positions of this initiating target sequence are 448.992 KB and 448.454 KB with a length of 0.022 KB. The identifier number of the terminating target sequence (T2) is 4824a. The genomic start and stop positions of this terminating target sequence are 488.140 KB and 488.297 KB with a length of 0.158 KB.

This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name YER138W-A. The genomic start and stop positions of this gene are 449.470 KB and 449.574 KB with a length of 0.105 KB. (2) The gene that has the name YER139C. The genomic start and stop positions of this gene are 450.558 KB and 453.230 KB with a length of 2.672 KB. (3) The gene that has the name YER140W. The genomic start and stop positions of this gene are 451.560 KB and 453.230 KB with a length of 1.671 KB. (4) The gene that has the name COX15 and with a COG identifier of COG1612. The genomic start and stop positions of this gene are 453.454 KB and 454.914 KB with a length of 1.461 KB. (5) The gene that has the name MAG1 and with a COG identifier of COG0122. The genomic start and stop positions of this gene are 455.141 KB and 457.600 KB with a

length of 2.459 KB. (6) The gene that has the name DDI1. The genomic start and stop positions of this gene are 456.314 KB and 457.600 KB with a length of 1.287 KB. (7) The gene that has the name UBP5. The genomic start and stop positions of this gene are 457.801 KB and 460.218 KB with a length of 2.418 KB. (8) The gene that has the name FTR1 and with a COG identifier of COG0672. The genomic start and stop positions of this gene are 460.521 KB and 466.020 KB with a length of 5.499 KB. (9) The gene that has the name LSM5 and with a COG identifier of COG1958. The genomic start and stop positions of this gene are 462.580 KB and 462.861 KB with a length of 0.282 KB. (10) The gene that has the name YER147C. The genomic start and stop positions of this gene are 464.837 KB and 462.963 KB with a length of 1.875 KB. (11) The gene that has the name SPT15 and with a COG identifier of COG2101. The genomic start and stop positions of this gene are 465.298 KB and 466.020 KB with a length of 0.723 KB. (12) The gene that has the name PEA2. The genomic start and stop positions of this gene are 466.203 KB and 468.811 KB with a length of 2.608 KB. (13) The gene that has the name SPI1. The genomic start and stop positions of this gene are 468.365 KB and 468.811 KB with a length of 0.447 KB. (14) The gene that has the name No_Name. The genomic start and stop positions of this gene are 469.452 KB and 469.525 KB with a length of 0.074 KB. (15) The gene that has the name UBP3. The genomic start and stop positions of this gene are 469.681 KB and 472.419 KB with a length of 2.739 KB. (16) The gene that has the name YER152C and with a COG identifier of COG1167. The genomic start and stop positions of this gene are 472.652 KB and 482.843 KB with a length of 10.191 KB. (17) The gene that has the name PET122. The genomic start and stop positions of this gene are 474.800 KB and 474.036 KB with a length of 0.765 KB. (18) The gene that has the name OXA1 and with a COG identifier of

COG0706. The genomic start and stop positions of this gene are 475.015 KB and 476.223 KB with a length of 1.209 KB. (19) The gene that has the name BEM2. The genomic start and stop positions of this gene are 482.843 KB and 476.340 KB with a length of 6.504 KB. (20) The gene that has the name YER156C. The genomic start and stop positions of this gene are 483.320 KB and 487.188 KB with a length of 3.868 KB. (21) The gene that has the name SEC34. The genomic start and stop positions of this gene are 484.783 KB and 487.188 KB with a length of 2.406 KB. (22) The gene that has the name No_Name. The genomic start and stop positions of this gene are 487.326 KB and 487.397 KB with a length of 0.072 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 4751 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 448.992 KB and 448.454 KB with a length of 0.539 KB. (2) The connectron that has the identifier 4754 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 449.315 KB and 449.003 KB with a length of 0.313 KB. (3) The connectron that has the identifier 4755 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 449.482 KB and 449.317 KB with a length of 0.166 KB. (4) The connectron that has the identifier 4759 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 449.490 KB and 449.563 KB with a length of 0.074 KB. (5) The connectron that has the identifier 4762 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 449.563 KB and 449.490 KB with a length of 0.074 KB. (6) The connectron that has the identifier 4768 is on

chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 453.923 KB and 453.909 KB with a length of 0.015 KB. (7) The connectron that has the identifier 4769 is on chromosome 5 in the negative direction.

5 The genomic start and stop positions of this connectron are 453.942 KB and 453.928 KB with a length of 0.015 KB. (8) The connectron that has the identifier 4779 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 463.990 KB and 464.004 KB with a length of

10 0.015 KB. (9) The connectron that has the identifier 4780 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 464.010 KB and 464.024 KB with a length of 0.015 KB. (10) The connectron that has the identifier 4785 is on chromosome 5 in the negative direction.

15 The genomic start and stop positions of this connectron are 469.530 KB and 469.451 KB with a length of 0.080 KB. (11) The connectron that has the identifier 4788 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 469.452 KB and 469.531 KB with a length of

20 0.080 KB. (12) The connectron that has the identifier 4795 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 478.412 KB and 478.426 KB with a length of 0.015 KB. (13) The connectron that has the identifier 4796 is on chromosome 5 in the positive direction.

25 The genomic start and stop positions of this connectron are 478.436 KB and 478.450 KB with a length of 0.015 KB. (14) The connectron that has the identifier 4797 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 481.812 KB and 481.782 KB with a length of

30 0.031 KB. (15) The connectron that has the identifier 4799 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 482.690 KB and 482.676 KB

with a length of 0.015 KB. (16) The connectron that has the identifier 4800 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 482.715 KB and 482.701 KB with a length of 0.015 KB. (17) The connectron that has the identifier 4803 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 485.113 KB and 485.099 KB with a length of 0.015 KB. (18) The connectron that has the identifier 4804 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 485.134 KB and 485.119 KB with a length of 0.016 KB. (19) The connectron that has the identifier 4807 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 487.375 KB and 487.397 KB with a length of 0.023 KB. (20) The connectron that has the identifier 4808 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 487.400 KB and 487.415 KB with a length of 0.016 KB. (21) The connectron that has the identifier 4809 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 487.848 KB and 487.830 KB with a length of 0.019 KB. (22) The connectron that has the identifier 4810 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 487.830 KB and 487.848 KB with a length of 0.019 KB. (23) The connectron that has the identifier 4813 is on chromosome 5 in the negative direction. The genomic start and stop positions of this connectron are 488.016 KB and 487.850 KB with a length of 0.167 KB. (24) The connectron that has the identifier 4814 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 487.850 KB and 488.016 KB with a length of 0.022 KB. (25) The connectron that has the identifier 4817 is on chromosome 5 in the negative direction.

The genomic start and stop positions of this connectron are 488.137 KB and 488.024 KB with a length of 0.114 KB. (26) The connectron that has the identifier 4818 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 488.024 KB and 488.068 KB with a length of 0.045 KB. (27) The connectron that has the identifier 4821 is on chromosome 5 in the positive direction. The genomic start and stop positions of this connectron are 488.069 KB and 488.137 KB with a length of 0.069 KB.

10

Addition of a Synthetic Connectron of Type 14 from Table 2

15 A synthetic virtual connectron of type 14 in which the C1 and C2 are natural elements, the T1 is a synthetic element and the T2 is a natural element can be introduced into the *Halobacterium* sp. genome by modifying the DNA double-strand sequences at 734.750kb through 734.942kb for a length of 0.193kb.

20

To create this example of a synthetic connectron of type 15 the T1 sequence for natural connectron 6627 (old position 733.018kb through 733.210kb) was copied into the new position stated above.

25

Connectron 7341 is an example of a transient connectron. It is described as

30

		C1/C2				T1-T2		
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type	
2587	1	6612	6612	1	6627	6852	transient	

The C1/C2 source of the transient connectron 7341 is represented in Table 1 as

5 Type Num Jobno Chr Start Stop Length GeneName
 CPT 6612 1 1 732.401 732.534 .134 OS-> |

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB). The symbol OS-> occurs because there is another connectron formed by this C1/C2 that happens to be a one-shot connectron.

20 The T1-T2 target of the transient connectron 7341 as shown in Table 1 is represented as

25 Type Num Jobno Chr Start Stop Length GeneName
 TP 6644a 1 1 734.750 734.942 .193 *-*
 GG 6646 1 1 735.009 735.881 .873 Group0493 |
 CNT 6647 1 1 735.364 735.378 .015 OS-> |
 TN 6648 1 1 735.364 735.378 .015 *-*
 CNT 6649 1 1 735.389 735.403 .015 --> |
 CNT 6650 1 1 735.753 735.767 .015 --> |
 30 CNT 6651 1 1 735.775 735.789 .015 --> |
 GG 6652 1 1 735.910 737.544 1.634 Group0494 |
 TN 6653 1 1 735.969 735.984 .016 *-*
 TN 6654 1 1 736.126 736.140 .015 *-*
 CPT 6655 1 1 736.325 736.339 .015 --> |
 35 TN 6656 1 1 736.327 736.342 .016 *-*
 CPT 6657 1 1 736.345 736.359 .015 --> |
 TP 6658 1 1 736.903 736.917 .015 *-*
 TN 6659 1 1 737.233 737.247 .015 *-*

	TP	6660	1	1	737.271	737.285	.015	*-+
	TN	6661	1	1	737.331	737.346	.016	*-+
	GG	6662	1	1	737.643	737.972	.330	Group0495
	TN	6663	1	1	737.752	737.766	.015	*-+
5	CNT	6664	1	1	737.752	737.782	.031	-->
	TP	6665	1	1	737.761	737.775	.015	*-+
	TN	6666	1	1	738.049	738.063	.015	*-+
	GG	6667	1	1	738.107	739.835	1.728	Group0496
	TN	6668	1	1	738.122	738.136	.015	*-+
10	TP	6669	1	1	738.122	738.136	.015	*-+
	TP	6670	1	1	738.425	738.439	.015	*-+
	TP	6671	1	1	738.503	738.517	.015	*-+
	CNT	6672	1	1	738.517	738.562	.046	-->
	TN	6673	1	1	738.544	738.559	.016	*-+
15	TN	6674	1	1	738.862	738.878	.017	*-+
	TP	6675	1	1	738.862	738.878	.017	*-+
	CNT	6676	1	1	738.975	738.989	.015	-->)
	CNT	6677	1	1	738.992	739.007	.016	-->
	TN	6678	1	1	739.107	739.122	.016	*-+
20	GN	6679	1	1	739.248	739.835	.588	cheC1
	TP	6680	1	1	739.435	739.449	.015	*-+
	TN	6681	1	1	739.685	739.707	.023	*-+
	TN	6682	1	1	739.761	739.775	.015	*-+
	GG	6683	1	1	739.838	741.844	2.007	Group0497
25	TN	6684	1	1	739.849	739.863	.015	*-+
	TP	6685	1	1	740.345	740.360	.016	*-+
	TN	6686	1	1	740.362	740.376	.015	*-+
	TP	6687	1	1	740.611	740.625	.015	*-+
	TN	6688	1	1	741.100	741.116	.017	*-+
30	TP	6689	1	1	741.101	741.132	.032	*-+
	TN	6690	1	1	741.218	741.232	.015	*-+
	CNT	6691	1	1	741.352	741.368	.017	-->
	TP	6692	1	1	741.354	741.376	.023	*-+
	TN	6693	1	1	741.354	741.380	.027	*-+
35	CNT	6694	1	1	741.374	741.388	.015	-->
	TN	6695	1	1	741.401	741.417	.017	*-+
	CNT	6696	1	1	741.519	741.533	.015	-->
	CNT	6697	1	1	741.538	741.552	.015	-->
	TN	6698	1	1	741.538	741.552	.015	*-+
40	TN	6699	1	1	741.561	741.575	.015	*-+
	GG	6700	1	1	741.846	743.248	1.403	Group0498
	TN	6701	1	1	741.924	741.942	.019	*-+
	TN	6702	1	1	742.194	742.208	.015	*-+
	TP	6703	1	1	742.618	742.632	.015	*-+
45	TN	6704	1	1	742.943	742.957	.015	*-+
	GG	6705	1	1	743.295	743.831	.537	Group0499
	TP	6706	1	1	743.730	743.748	.019	*-+
	GG	6707	1	1	743.896	744.489	.594	Group0500

	TN	6708	1	1	743.916	743.930	.015	*-+
	GG	6709	1	1	744.606	745.511	.906	Group0501
	TN	6710	1	1	744.950	744.964	.015	*-+
	TN	6711	1	1	745.047	745.061	.015	*-+
5	GG	6712	1	1	745.648	746.763	1.116	Group0502
	CPT	6713	1	1	745.865	745.879	.015	-->
	TN	6714	1	1	745.865	745.879	.015	*-+
	CPT	6715	1	1	745.888	745.902	.015	-->
	CPT	6716	1	1	746.140	746.155	.016	-->
10	TN	6717	1	1	746.153	746.175	.023	*-+
	TP	6718	1	1	746.157	746.175	.019	*-+
	CPT	6719	1	1	746.162	746.176	.015	-->
	TN	6720	1	1	746.229	746.243	.015	*-+
	CNT	6721	1	1	746.229	746.259	.031	-->
15	TN	6722	1	1	746.271	746.285	.015	*-+
	TP	6723	1	1	746.356	746.380	.025	*-+
	TN	6724	1	1	746.361	746.380	.020	*-+
	TN	6725	1	1	746.386	746.400	.015	*-+
	CPT	6726	1	1	746.453	746.467	.015	-->
20	TN	6727	1	1	746.453	746.472	.020	*-+
	TP	6728	1	1	746.457	746.475	.019	*-+
	CPT	6729	1	1	746.469	746.483	.015	-->
	TP	6730	1	1	746.528	746.545	.018	*-+
	TN	6731	1	1	746.532	746.556	.025	*-+
25	GG	6732	1	1	746.843	748.851	2.008	Group0503
	CNT	6733	1	1	746.905	746.919	.015	-->
	CNT	6734	1	1	746.927	746.941	.015	-->
	GN	6735	1	1	747.151	748.605	1.455	VNG0983C
	TN	6736	1	1	747.260	747.274	.015	*-+
30	TP	6737	1	1	747.475	747.489	.015	*-+
	TN	6738	1	1	747.547	747.571	.025	*-+
	TN	6739	1	1	747.934	747.948	.015	*-+
	TP	6740	1	1	747.936	747.950	.015	*-+
	TN	6741	1	1	748.130	748.144	.015	*-+
35	TP	6742	1	1	749.157	749.172	.016	*-+
	TN	6743	1	1	749.375	749.389	.015	*-+
	GG	6744	1	1	749.392	759.277	9.885	Group0504
	CNT	6745	1	1	759.509	759.552	.044	-->
	TP	6746	1	1	759.509	760.014	.506	*-+
40	TN	6747	1	1	759.528	760.031	.504	*-+
	GG	6748	1	1	759.667	762.487	2.820	Group0505
	GP	6749	1	1	760.682	762.487	1.806	boa4
	CPT	6750	1	1	760.774	760.789	.016	-->
	CPT	6751	1	1	760.798	760.814	.017	-->
45	TN	6752	1	1	760.875	760.889	.015	*-+
	CPT	6753	1	1	760.878	760.892	.015	-->
	CPT	6754	1	1	760.897	760.912	.016	-->
	CPT	6755	1	1	761.496	761.510	.015	-->

5	CPT	6756	1	1	761.516	761.533	.018	-->	
	CPT	6757	1	1	761.542	761.557	.016	-->	
	TN	6758	1	1	761.542	761.557	.016	*-+	
	CPT	6759	1	1	761.576	761.597	.022	-->	
	CPT	6760	1	1	761.601	761.617	.017	-->	
	TN	6761	1	1	761.754	761.768	.015	*-+	
	CPT	6762	1	1	761.933	761.950	.018	-->	
	TP	6763	1	1	761.933	761.950	.018	*-+	
10	CPT	6764	1	1	761.953	761.968	.016	-->	
	TN	6765	1	1	762.423	762.437	.015	*-+	
	GG	6766	1	1	762.609	764.612	2.004	Group0506	
	TN	6767	1	1	762.874	762.900	.027	*-+	
15	TN	6768	1	1	762.946	762.960	.015	*-+	
	TN	6769	1	1	763.108	763.122	.015	*-+	
	TN	6770	1	1	763.273	763.304	.032	*-+	
	CPT	6771	1	1	763.283	763.304	.022	-->	
20	TN	6772	1	1	763.306	763.320	.015	*-+	
	CPT	6773	1	1	763.306	763.321	.016	-->	
	CPT	6774	1	1	763.346	763.360	.015	-->	
	TN	6775	1	1	763.351	763.365	.015	*-+	
25	TP	6776	1	1	763.351	763.365	.015	*-+	
	CPT	6777	1	1	763.362	763.376	.015	-->	
	TP	6778	1	1	763.391	763.407	.017	*-+	
	TN	6779	1	1	763.843	763.857	.015	*-+	
30	TP	6780	1	1	763.843	763.857	.015	*-+	
	CNT	6781	1	1	763.965	763.986	.022	-->	
	CPT	6782	1	1	763.965	763.995	.031	-->	
	CNT	6783	1	1	763.990	764.011	.022	-->	
35	CPT	6784	1	1	764.000	764.015	.016	-->	
	CNT	6785	1	1	764.075	764.089	.015	-->	
	CNT	6786	1	1	764.093	764.108	.016	-->	
	CPT	6787	1	1	764.156	764.171	.016	-->	
40	CNT	6788	1	1	764.156	764.177	.022	OS->	
	TN	6789	1	1	764.156	764.177	.022	*-+	
	CNT	6790	1	1	764.181	764.195	.015	-->	
	TP	6791	1	1	764.181	764.201	.021	*-+	
45	CPT	6792	1	1	764.181	764.204	.024	-->	
	CPT	6793	1	1	764.213	764.227	.015	-->	
	TP	6794	1	1	764.309	764.328	.020	*-+	
	TN	6795	1	1	764.312	764.326	.015	*-+	
50	TN	6796	1	1	764.383	764.397	.015	*-+	
	TP	6797	1	1	764.530	764.545	.016	*-+	
	TN	6798	1	1	764.530	764.548	.019	*-+	
	GG	6799	1	1	764.619	765.629	1.011	Group0507	
55	CPT	6800	1	1	764.791	764.808	.018	-->	
	CNT	6801	1	1	764.794	764.813	.020	OS->	
	TN	6802	1	1	764.794	764.832	.039	*-+	
	CPT	6803	1	1	764.810	764.826	.017	-->	

	CNT	6804	1	1	764.818	764.832	.015	-->	
	CPT	6805	1	1	764.831	764.853	.023	-->	
	CPT	6806	1	1	764.856	764.870	.015	-->	
	CNT	6807	1	1	764.984	764.998	.015	OS->	
5	TN	6808	1	1	764.984	765.014	.031	*-+	
	CNT	6809	1	1	765.000	765.014	.015	-->	
	TN	6810	1	1	765.075	765.089	.015	*-+	
	CNT	6811	1	1	765.431	765.446	.016	-->	
	CNT	6812	1	1	765.456	765.473	.018	-->	
10	CNT	6813	1	1	765.479	765.494	.016	-->	
	TN	6814	1	1	765.508	765.523	.016	*-+	
	TP	6815	1	1	765.573	765.587	.015	*-+	
	GG	6816	1	1	765.775	766.044	.270	Group0508	
	TN	6817	1	1	765.822	765.837	.016	*-+	
15	TP	6818	1	1	766.162	766.176	.015	*-+	
	TN	6819	1	1	766.432	766.447	.016	*-+	
	GG	6820	1	1	766.603	766.812	.210	Group0509	
	CNT	6821	1	1	766.635	766.653	.019	OS->	
	TN	6822	1	1	766.635	766.653	.019	*-+	
20	CNT	6823	1	1	766.655	766.675	.021	-->	
	TN	6824	1	1	766.863	766.878	.016	*-+	
	GG	6825	1	1	766.955	768.538	1.584	Group0510	
	TN	6826	1	1	767.682	767.700	.019	*-+	
	TP	6827	1	1	767.831	767.845	.015	*-+	
25	TN	6828	1	1	768.028	768.048	.021	*-+	
	TP	6829	1	1	768.033	768.049	.017	*-+	
	TN	6830	1	1	768.377	768.391	.015	*-+	
	GG	6831	1	1	768.965	769.882	.918	Group0511	
	TN	6832	1	1	769.502	769.516	.015	*-+	
30	TN	6833	1	1	769.541	769.555	.015	*-+	
	TP	6834	1	1	769.559	769.573	.015	*-+	
	GG	6835	1	1	769.965	770.189	.225	Group0512	
	TN	6836	1	1	770.120	770.134	.015	*-+	
	GG	6837	1	1	770.194	770.406	.213	Group0513	
35	CPT	6838	1	1	770.226	770.240	.015	-->	
	CPT	6839	1	1	770.251	770.265	.015	-->	
	TP	6840	1	1	770.251	770.268	.018	*-+	
	CPT	6841	1	1	770.347	770.363	.017	-->	
	CPT	6842	1	1	770.365	770.379	.015	-->	
40	GG	6843	1	1	770.516	771.546	1.030	Group0514	
	TN	6844	1	1	771.564	772.071	.508	*-+	
	CNT	6845	1	1	771.564	772.086	.523	-->	
	TP	6846	1	1	771.583	772.084	.502	*-+	
	GG	6847	1	1	771.722	771.925	.204	Group0515	
45	TN	6848	1	1	772.963	772.977	.015	*-+	
	TP	6849	1	1	773.358	773.387	.030	*-+	
	GG	6850	1	1	773.360	773.950	.591	Group0516	
	CPT	6851	1	1	773.399	773.483	.085	OS->	

TP 6852 1 1 773.399 773.483 .085 **

The "Type" descriptor of the T1 (Id number 6644a) is "TP" showing that is T1 target is on the negative strand of the double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 6852) also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Group0493 (Id number 6646) has the type descriptor "GG". The same is true for the group headers through to Group0516 (Id number 6847).

Group0493

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG0964C	COG2469	S	1 positive	735.009	735.881	.873

Group0494

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG0965C	COG2469	S	1 negative	735.910	736.773	.864
cheR	COG1352	N	1 negative	736.840	737.544	.705

Group0495

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
5	cheD	COG1871	N	1 negative	737.643	737.972	.330

Group0496

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
10	VNG0969H	COG1776	N	1 negative	738.107	739.246	1.140
	cheC1	COG1776	N	1 negative	739.248	739.835	.588

Group0497

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
15	cheA	COG0643	N	1 negative	739.838	741.844	2.007

Group0498

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
20	cheB	COG2201	N	1 negative	741.846	743.248	1.403

Group0499

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
25	cheW1	COG0835	N	1 negative	743.295	743.831	.537

Group0500

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
30	VNG0978H		1	negative	743.896	744.489	.594

Group0501

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
35	VNG0979H		1	positive	744.606	745.511	.906

Group0502

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
40	VNG0981C	COG0436	E	1 positive	745.648	746.763	1.116

Group0503

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
45	VNG0982C	COG1873	S	1 positive	746.843	747.133	.291
	VNG0983C	COG0618	R	1 negative	747.151	748.605	1.455
	tRNA-Lys		1	positive	748.778	748.851	.074

Group0504

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
5	VNG0985H		1	positive	749.392	751.398	2.007	
	VNG0986H		1	positive	752.276	752.803	.528	
	VNG0987H		1	positive	753.131	753.547	.417	
	VNG0988H		1	positive	754.149	754.391	.243	
10	VNG0989C	COG0582	L	1	negative	754.459	755.481	1.023
	VNG0990H		1	positive	756.010	756.183	.174	
	VNG0991H		1	negative	756.675	757.016	.342	
	VNG0992H		1	negative	757.409	758.119	.711	
	VNG0993H		1	positive	758.465	759.277	.813	

15 Group0505

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
	VNG0994H		1	negative	759.667	759.870	.204	
	VNG0995H		1	positive	760.365	760.553	.189	
20	boa4	COG3413	R	1	positive	760.682	762.487	1.806

Group0506

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
25	acs2	COG0365	I	1	positive	762.609	764.612	2.004

Group0507

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
30	yaj02	COG0667	C	1	negative	764.619	765.629	1.011

Group0508

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
35	VNG0999H		1	negative	765.775	766.044	.270

Group0509

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
40	VNG1000H	COG3205	S	1	positive	766.603	766.812	.210

Group0510

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
45	quaB	COG0516	F	1	negative	766.955	768.538	1.584

Group0511

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG1002H		1	positive	768.965	769.882	.918

Group0512

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG1003H		1	positive	769.965	770.189	.225

Group0513

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG1005H		1	negative	770.194	770.406	.213

Group0514

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
tRNA-Trp		1	positive	770.516	770.691	.176
VNG1006H		1	positive	770.827	771.546	.720

Group0515

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
VNG1007H		1	negative	771.722	771.925	.204

Group0516

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
flaA1a	COG1681	N	1	positive	773.360	773.950	.591

All of the data for the transient connectron 7341 are pulled together in the following table that is the "terse" description of the connectron.

Connectron Relationships - Global_Id Type

7341	transient
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Control Sequences - Direction Chromosome C1/C2_Id Start Stop Length

positive	1	6612	732.401	732.534	.134
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Trigger Gene - Name COG_Id Start Stop Length

flaB1	COG1681	731.799	732.380	.582
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Target Sequences - Direction Chromosome T1_Id Start Stop Length

positive 1 6644a 734.750 734.942 .193

T2_Id Start Stop Length
6852 773.399 773.483 .085

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Controlled Genes

	Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
	1	1	Group0493	VNG0964C	COG2469	positive	735.009	735.881	.873
	2	1	Group0494	VNG0965C	COG2469	positive	735.910	737.544	1.634
10	3	1	Group0494	cheR	COG1352	negative	737.544	736.840	.705
	4	1	Group0495	cheD	COG1871	positive	737.643	737.972	.330
	5	1	Group0496	VNG0969H	COG1776	positive	738.107	739.835	1.728
	6	1	Group0496	cheC1	COG1776	negative	739.835	739.248	.588
	7	1	Group0497	cheA	COG0643	positive	739.838	741.844	2.007
15	8	1	Group0498	cheB	COG2201	positive	741.846	743.248	1.403
	9	1	Group0499	cheW1	COG0835	positive	743.295	743.831	.537
	10	1	Group0500	VNG0978H		positive	743.896	744.489	.594
	11	1	Group0501	VNG0979H		positive	744.606	745.511	.906
	12	1	Group0502	VNG0981C	COG0436	positive	745.648	746.763	1.116
20	13	1	Group0503	VNG0982C	COG1873	positive	746.843	748.851	2.008
	14	1	Group0503	VNG0983C	COG0618	negative	748.605	747.151	1.455
	15	1	Group0504	VNG0985H		positive	749.392	759.277	9.885
	16	1	Group0504	VNG0986H		positive	752.276	752.803	.528
	17	1	Group0504	VNG0987H		positive	753.131	753.547	.417
25	18	1	Group0504	VNG0988H		positive	754.149	754.391	.243
	19	1	Group0504	VNG0989C	COG0582	negative	755.481	754.459	1.023
	20	1	Group0504	VNG0990H		positive	756.010	756.183	.174
	21	1	Group0504	VNG0991H		negative	757.016	756.675	.342
	22	1	Group0504	VNG0992H		negative	758.119	757.409	.711
30	23	1	Group0504	VNG0993H		positive	758.465	759.277	.813
	24	1	Group0505	VNG0994H		positive	759.667	762.487	2.820
	25	1	Group0505	VNG0995H		positive	760.365	760.553	.189
	26	1	Group0505	boa4	COG3413	positive	760.682	762.487	1.806
35	27	1	Group0506	acs2	COG0365	positive	762.609	764.612	2.004
	28	1	Group0507	yajO2	COG0667	positive	764.619	765.629	1.011
	29	1	Group0508	VNG0999H		positive	765.775	766.044	.270
	30	1	Group0509	VNG1000H	COG3205	positive	766.603	766.812	.210
	31	1	Group0510	guaB	COG0516	positive	766.955	768.538	1.584
	32	1	Group0511	VNG1002H		positive	768.965	769.882	.918
40	33	1	Group0512	VNG1003H		positive	769.965	770.189	.225
	34	1	Group0513	VNG1005H		positive	770.194	770.406	.213
	35	1	Group0514	tRNA-Trp		positive	770.516	771.546	1.030
	36	1	Group0514	VNG1006H		positive	770.827	771.546	.720
	37	1	Group0515	VNG1007H		positive	771.722	771.925	.204
45	38	1	Group0516	flaA1a	COG1681	positive	773.360	773.950	.591

Controlled Connectrons

Local_Id Chromosome C1/C2_Id Direction Start Stop Length

5	1	1	6644	positive	734.735	734.749	.015
	2	1	6647	negative	735.378	735.364	.015
	3	1	6649	negative	735.403	735.389	.015
	4	1	6650	negative	735.767	735.753	.015
	5	1	6651	negative	735.789	735.775	.015
10	6	1	6655	positive	736.325	736.339	.015
	7	1	6657	positive	736.345	736.359	.015
	8	1	6664	negative	737.782	737.752	.031
	9	1	6672	negative	738.562	738.517	.046
	10	1	6676	negative	738.989	738.975	.015
15	11	1	6677	negative	739.007	738.992	.016
	12	1	6691	negative	741.368	741.352	.017
	13	1	6694	negative	741.388	741.374	.015
	14	1	6696	negative	741.533	741.519	.015
	15	1	6697	negative	741.552	741.538	.015
20	16	1	6713	positive	745.865	745.879	.015
	17	1	6715	positive	745.888	745.902	.015
	18	1	6716	positive	746.140	746.155	.016
	19	1	6719	positive	746.162	746.176	.015
	20	1	6721	negative	746.259	746.229	.031
25	21	1	6726	positive	746.453	746.467	.015
	22	1	6729	positive	746.469	746.483	.015
	23	1	6733	negative	746.919	746.905	.015
	24	1	6734	negative	746.941	746.927	.015
	25	1	6745	negative	759.552	759.509	.044
30	26	1	6750	positive	760.774	760.789	.016
	27	1	6751	positive	760.798	760.814	.017
	28	1	6753	positive	760.878	760.892	.015
	29	1	6754	positive	760.897	760.912	.016
	30	1	6755	positive	761.496	761.510	.015
35	31	1	6756	positive	761.516	761.533	.018
	32	1	6757	positive	761.542	761.557	.016
	33	1	6759	positive	761.576	761.597	.022
	34	1	6760	positive	761.601	761.617	.017
	35	1	6762	positive	761.933	761.950	.018
40	36	1	6764	positive	761.953	761.968	.016
	37	1	6771	positive	763.283	763.304	.022
	38	1	6773	positive	763.306	763.321	.016
	39	1	6774	positive	763.346	763.360	.015
	40	1	6777	positive	763.362	763.376	.015
45	41	1	6781	negative	763.986	763.965	.022
	42	1	6782	positive	763.965	763.995	.031
	43	1	6783	negative	764.011	763.990	.022
	44	1	6784	positive	764.000	764.015	.016
	45	1	6785	negative	764.089	764.075	.015
	46	1	6786	negative	764.108	764.093	.016
	47	1	6787	positive	764.156	764.171	.016
	48	1	6788	negative	764.177	764.156	.022

5	49	1	6790	negative	764.195	764.181	.015
	50	1	6792	positive	764.181	764.204	.024
	51	1	6793	positive	764.213	764.227	.015
	52	1	6800	positive	764.791	764.808	.018
	53	1	6801	negative	764.813	764.794	.020
	54	1	6803	positive	764.810	764.826	.017
	55	1	6804	negative	764.832	764.818	.015
	56	1	6805	positive	764.831	764.853	.023
	57	1	6806	positive	764.856	764.870	.015
10	58	1	6807	negative	764.998	764.984	.015
	59	1	6809	negative	765.014	765.000	.015
	60	1	6811	negative	765.446	765.431	.016
	61	1	6812	negative	765.473	765.456	.018
	62	1	6813	negative	765.494	765.479	.016
15	63	1	6821	negative	766.653	766.635	.019
	64	1	6823	negative	766.675	766.655	.021
	65	1	6838	positive	770.226	770.240	.015
	66	1	6839	positive	770.251	770.265	.015
	67	1	6841	positive	770.347	770.363	.017
20	68	1	6842	positive	770.365	770.379	.015
	69	1	6845	negative	772.086	771.564	.523
	70	1	6851	positive	773.399	773.483	.085

25

The verbose description of the transient connectron 7341 is:

In the Halobacterium sp. NRC-1 complete genome the transient connectron number 7341 is generated by the control sequence
30 (C1/C2) whose identifier number is 6612. This control sequence is on the positive strand of the genomic DNA of chromosome 1. The genomic start and stop positions of this control sequence are 732.401 KB and 732.534 KB with a length of 0.134 KB. Expression of the RNA for this connectron is triggered by the
35 promotion of the gene whose name is flaB1 and whose COG (Cluster of Orthologous Genes) identifier is COG1681. The genomic start and stop positions of this gene are 731.799 KB and 732.380 KB and with a length of 0.582 KB. This connectron causes
40 stabilization of a loop of DNA. The target sequences (T1-T2) are on the positive strand of the genomic DNA on chromosome 1.

The identifier number of the initiating target sequence (T1) is 6644a. The genomic start and stop positions of this initiating target sequence are 734.750 KB and 734.942 KB with a length of 0.193 KB. The identifier number of the terminating target
5 sequence (T2) is 6852. The genomic start and stop positions of this terminating target sequence are 773.399 KB and 773.483 KB with a length of 0.085 KB.

This connectron controls the modulation of the expression of the
10 following gene(s): (1) The gene that has the name VNG0964C and with a COG identifier of COG2469. The genomic start and stop positions of this gene are 735.009 KB and 735.881 KB with a length of 0.873 KB. (2) The gene that has the name VNG0965C and with a COG identifier of COG2469. The genomic start and stop
15 positions of this gene are 735.910 KB and 737.544 KB with a length of 1.634 KB. (3) The gene that has the name cheR and with a COG identifier of COG1352. The genomic start and stop positions of this gene are 737.544 KB and 736.840 KB with a length of 0.705 KB. (4) The gene that has the name cheD and with
20 a COG identifier of COG1871. The genomic start and stop positions of this gene are 737.643 KB and 737.972 KB with a length of 0.330 KB. (5) The gene that has the name VNG0969H and with a COG identifier of COG1776. The genomic start and stop positions of this gene are 738.107 KB and 739.835 KB with a
25 length of 1.728 KB. (6) The gene that has the name cheC1 and with a COG identifier of COG1776. The genomic start and stop positions of this gene are 739.835 KB and 739.248 KB with a length of 0.588 KB. (7) The gene that has the name cheA and with a COG identifier of COG0643. The genomic start and stop
30 positions of this gene are 739.838 KB and 741.844 KB with a length of 2.007 KB. (8) The gene that has the name cheB and with a COG identifier of COG2201. The genomic start and stop

positions of this gene are 741.846 KB and 743.248 KB with a length of 1.403 KB. (9) The gene that has the name *cheW1* and with a COG identifier of COG0835. The genomic start and stop positions of this gene are 743.295 KB and 743.831 KB with a length of 0.537 KB. (10) The gene that has the name VNG0978H. The genomic start and stop positions of this gene are 743.896 KB and 744.489 KB with a length of 0.594 KB. (11) The gene that has the name VNG0979H. The genomic start and stop positions of this gene are 744.606 KB and 745.511 KB with a length of 0.906 KB.

(12) The gene that has the name VNG0981C and with a COG identifier of COG0436. The genomic start and stop positions of this gene are 745.648 KB and 746.763 KB with a length of 1.116 KB. (13) The gene that has the name VNG0982C and with a COG identifier of COG1873. The genomic start and stop positions of this gene are 746.843 KB and 748.851 KB with a length of 2.008 KB. (14) The gene that has the name VNG0983C and with a COG identifier of COG0618. The genomic start and stop positions of this gene are 748.605 KB and 747.151 KB with a length of 1.455 KB. (15) The gene that has the name VNG0985H. The genomic start and stop positions of this gene are 749.392 KB and 759.277 KB with a length of 9.885 KB. (16) The gene that has the name VNG0986H. The genomic start and stop positions of this gene are 752.276 KB and 752.803 KB with a length of 0.528 KB. (17) The gene that has the name VNG0987H. The genomic start and stop positions of this gene are 753.131 KB and 753.547 KB with a length of 0.417 KB. (18) The gene that has the name VNG0988H. The genomic start and stop positions of this gene are 754.149 KB and 754.391 KB with a length of 0.243 KB. (19) The gene that has the name VNG0989C and with a COG identifier of COG0582. The genomic start and stop positions of this gene are 755.481 KB and 754.459 KB with a length of 1.023 KB. (20) The gene that has the name VNG0990H. The genomic start and stop positions of this

gene are 756.010 KB and 756.183 KB with a length of 0.174 KB.

(21) The gene that has the name VNG0991H. The genomic start and stop positions of this gene are 757.016 KB and 756.675 KB with a length of 0.342 KB. (22) The gene that has the name VNG0992H.

5 The genomic start and stop positions of this gene are 758.119 KB and 757.409 KB with a length of 0.711 KB. (23) The gene that has the name VNG0993H. The genomic start and stop positions of this gene are 758.465 KB and 759.277 KB with a length of 0.813 KB.

(24) The gene that has the name VNG0994H. The genomic start and stop positions of this gene are 759.667 KB and 762.487 KB with a length of 2.820 KB. (25) The gene that has the name VNG0995H.

The genomic start and stop positions of this gene are 760.365 KB and 760.553 KB with a length of 0.189 KB. (26) The gene that has the name *boa4* and with a COG identifier of COG3413. The genomic

15 start and stop positions of this gene are 760.682 KB and 762.487 KB with a length of 1.806 KB. (27) The gene that has the name *acs2* and with a COG identifier of COG0365. The genomic start and stop positions of this gene are 762.609 KB and 764.612 KB with a length of 2.004 KB. (28) The gene that has the name *yajO2*

20 and with a COG identifier of COG0667. The genomic start and stop positions of this gene are 764.619 KB and 765.629 KB with a length of 1.011 KB. (29) The gene that has the name VNG0999H.

The genomic start and stop positions of this gene are 765.775 KB and 766.044 KB with a length of 0.270 KB. (30) The gene that has

25 the name VNG1000H and with a COG identifier of COG3205. The genomic start and stop positions of this gene are 766.603 KB and 766.812 KB with a length of 0.210 KB. (31) The gene that has the name *guaB* and with a COG identifier of COG0516. The genomic

start and stop positions of this gene are 766.955 KB and 768.538 KB with a length of 1.584 KB. (32) The gene that has the name

30 VNG1002H. The genomic start and stop positions of this gene are 768.965 KB and 769.882 KB with a length of 0.918 KB. (33) The

gene that has the name VNG1003H. The genomic start and stop positions of this gene are 769.965 KB and 770.189 KB with a length of 0.225 KB. (34) The gene that has the name VNG1005H. The genomic start and stop positions of this gene are 770.194 KB and 770.406 KB with a length of 0.213 KB. (35) The gene that has the name tRNA-Trp. The genomic start and stop positions of this gene are 770.516 KB and 771.546 KB with a length of 1.030 KB. (36) The gene that has the name VNG1006H. The genomic start and stop positions of this gene are 770.827 KB and 771.546 KB with a length of 0.720 KB. (37) The gene that has the name VNG1007H. The genomic start and stop positions of this gene are 771.722 KB and 771.925 KB with a length of 0.204 KB. (38) The gene that has the name flaAla and with a COG identifier of COG1681. The genomic start and stop positions of this gene are 773.360 KB and 773.950 KB with a length of 0.591 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 6644 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 734.735 KB and 734.749 KB with a length of 0.015 KB. (2) The connectron that has the identifier 6647 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 735.378 KB and 735.364 KB with a length of 0.015 KB. (3) The connectron that has the identifier 6649 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 735.403 KB and 735.389 KB with a length of 0.015 KB. (4) The connectron that has the identifier 6650 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 735.767 KB and 735.753 KB with a length of 0.015 KB. (5) The connectron that has the identifier 6651 is on chromosome 1 in

the negative direction. The genomic start and stop positions of this connectron are 735.789 KB and 735.775 KB with a length of 0.015 KB. (6) The connectron that has the identifier 6655 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 736.325 KB and 736.339 KB with a length of 0.015 KB. (7) The connectron that has the identifier 6657 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 736.345 KB and 736.359 KB with a length of 0.015 KB. (8) The connectron that has the identifier 6664 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 737.782 KB and 737.752 KB with a length of 0.031 KB. (9) The connectron that has the identifier 6672 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 738.562 KB and 738.517 KB with a length of 0.046 KB. (10) The connectron that has the identifier 6676 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 738.989 KB and 738.975 KB with a length of 0.015 KB. (11) The connectron that has the identifier 6677 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 739.007 KB and 738.992 KB with a length of 0.016 KB. (12) The connectron that has the identifier 6691 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 741.368 KB and 741.352 KB with a length of 0.017 KB. (13) The connectron that has the identifier 6694 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 741.388 KB and 741.374 KB with a length of 0.015 KB. (14) The connectron that has the identifier 6696 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 741.533 KB and 741.519 KB with a length of

0.015 KB. (15) The connectron that has the identifier 6697 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 741.552 KB and 741.538 KB with a length of 0.015 KB. (16) The connectron that has the identifier 6713 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 745.865 KB and 745.879 KB with a length of 0.015 KB. (17) The connectron that has the identifier 6715 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 745.888 KB and 745.902 KB with a length of 0.015 KB. (18) The connectron that has the identifier 6716 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 746.140 KB and 746.155 KB with a length of 0.016 KB. (19) The connectron that has the identifier 6719 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 746.162 KB and 746.176 KB with a length of 0.015 KB. (20) The connectron that has the identifier 6721 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 746.259 KB and 746.229 KB with a length of 0.031 KB. (21) The connectron that has the identifier 6726 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 746.453 KB and 746.467 KB with a length of 0.015 KB. (22) The connectron that has the identifier 6729 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 746.469 KB and 746.483 KB with a length of 0.015 KB. (23) The connectron that has the identifier 6733 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 746.919 KB and 746.905 KB with a length of 0.015 KB. (24) The connectron that has the identifier 6734 is on chromosome 1 in the negative direction. The genomic start and

stop positions of this connectron are 746.941 KB and 746.927 KB with a length of 0.015 KB. (25) The connectron that has the identifier 6745 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are

5 759.552 KB and 759.509 KB with a length of 0.044 KB. (26) The connectron that has the identifier 6750 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 760.774 KB and 760.789 KB with a length of 0.016 KB. (27) The connectron that has the identifier 6751 is on

10 chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 760.798 KB and 760.814 KB with a length of 0.017 KB. (28) The connectron that has the identifier 6753 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are

15 760.878 KB and 760.892 KB with a length of 0.015 KB. (29) The connectron that has the identifier 6754 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 760.897 KB and 760.912 KB with a length of 0.016 KB. (30) The connectron that has the identifier 6755 is on

20 chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.496 KB and 761.510 KB with a length of 0.015 KB. (31) The connectron that has the identifier 6756 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are

25 761.516 KB and 761.533 KB with a length of 0.018 KB. (32) The connectron that has the identifier 6757 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.542 KB and 761.557 KB with a length of 0.016 KB. (33) The connectron that has the identifier 6759 is on

30 chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.576 KB and 761.597 KB with a length of 0.022 KB. (34) The connectron that has the

identifier 6760 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.601 KB and 761.617 KB with a length of 0.017 KB. (35) The connectron that has the identifier 6762 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.933 KB and 761.950 KB with a length of 0.018 KB. (36) The connectron that has the identifier 6764 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 761.953 KB and 761.968 KB with a length of 0.016 KB. (37) The connectron that has the identifier 6771 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.283 KB and 763.304 KB with a length of 0.022 KB. (38) The connectron that has the identifier 6773 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.306 KB and 763.321 KB with a length of 0.016 KB. (39) The connectron that has the identifier 6774 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.346 KB and 763.360 KB with a length of 0.015 KB. (40) The connectron that has the identifier 6777 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.362 KB and 763.376 KB with a length of 0.015 KB. (41) The connectron that has the identifier 6781 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 763.986 KB and 763.965 KB with a length of 0.022 KB. (42) The connectron that has the identifier 6782 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 763.965 KB and 763.995 KB with a length of 0.031 KB. (43) The connectron that has the identifier 6783 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are

764.011 KB and 763.990 KB with a length of 0.022 KB. (44) The connectron that has the identifier 6784 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.000 KB and 764.015 KB with a length of 0.016 KB. (45) The connectron that has the identifier 6785 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.089 KB and 764.075 KB with a length of 0.015 KB. (46) The connectron that has the identifier 6786 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.108 KB and 764.093 KB with a length of 0.016 KB. (47) The connectron that has the identifier 6787 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.156 KB and 764.171 KB with a length of 0.016 KB. (48) The connectron that has the identifier 6788 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.177 KB and 764.156 KB with a length of 0.022 KB. (49) The connectron that has the identifier 6790 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.195 KB and 764.181 KB with a length of 0.015 KB. (50) The connectron that has the identifier 6792 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.181 KB and 764.204 KB with a length of 0.024 KB. (51) The connectron that has the identifier 6793 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.213 KB and 764.227 KB with a length of 0.015 KB. (52) The connectron that has the identifier 6800 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.791 KB and 764.808 KB with a length of 0.018 KB. (53) The connectron that has the identifier 6801 is on chromosome 1 in

the negative direction. The genomic start and stop positions of this connectron are 764.813 KB and 764.794 KB with a length of 0.020 KB. (54) The connectron that has the identifier 6803 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.810 KB and 764.826 KB with a length of 0.017 KB. (55) The connectron that has the identifier 6804 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.832 KB and 764.818 KB with a length of 0.015 KB. (56) The connectron that has the identifier 6805 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.831 KB and 764.853 KB with a length of 0.023 KB. (57) The connectron that has the identifier 6806 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 764.856 KB and 764.870 KB with a length of 0.015 KB. (58) The connectron that has the identifier 6807 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 764.998 KB and 764.984 KB with a length of 0.015 KB. (59) The connectron that has the identifier 6809 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 765.014 KB and 765.000 KB with a length of 0.015 KB. (60) The connectron that has the identifier 6811 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 765.446 KB and 765.431 KB with a length of 0.016 KB. (61) The connectron that has the identifier 6812 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 765.473 KB and 765.456 KB with a length of 0.018 KB. (62) The connectron that has the identifier 6813 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 765.494 KB and 765.479 KB with a length of

0.016 KB. (63) The connectron that has the identifier 6821 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 766.653 KB and 766.635 KB with a length of 0.019 KB. (64) The connectron that has the identifier 6823 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 766.675 KB and 766.655 KB with a length of 0.021 KB. (65) The connectron that has the identifier 6838 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 770.226 KB and 770.240 KB with a length of 0.015 KB. (66) The connectron that has the identifier 6839 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 770.251 KB and 770.265 KB with a length of 0.015 KB. (67) The connectron that has the identifier 6841 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 770.347 KB and 770.363 KB with a length of 0.017 KB. (68) The connectron that has the identifier 6842 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 770.365 KB and 770.379 KB with a length of 0.015 KB. (69) The connectron that has the identifier 6845 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 772.086 KB and 771.564 KB with a length of 0.523 KB. (70) The connectron that has the identifier 6851 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 773.399 KB and 773.483 KB with a length of 0.085 KB.

Addition of a Synthetic Virtual Connectron of Type 15 from Table 2

5 A synthetic virtual connectron of type 15 in which the C1 and C2 are natural elements, the T1 is a natural element and the T2 is a synthetic element can be introduced into the *P. aeruginosa* genome by modifying the DNA double-strand sequences at 4838.155kb through 4838.323kb for a length of 0.169kb.

10

To create this example of a synthetic connectron of type 14 the T2 sequence for natural connectron 23295 (old position 4848.679kb through 4939.847kb) was copied into the new position stated above.

15

Connectron 28739 is an example of a synthetic transient connectron. It is described as

20

		C1/C2		T1-T2			
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
28739	1	53464	53464	1	53531	53569	transient

The C1/C2 source of the transient connectron 28739 is represented in table 1 as

25

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
CPT	53464	1	1	4832.718	4832.838	.121	-->

30

The "Type" descriptor of this transient C1/C2 connectron source is "CPT". The letter "P" indicates that the C1/C2 connectron source occurs on the positive strand of the double-stranded DNA of the genome. The letter "N" in this place would indicate a

C1/C2 connectron source on the negative strand of the genomic DNA. The letter "T" in this descriptor indicates a "transient" connectron. Similarly, the letter "P" would indicate a permanent connectron that is shown in a later example. The
5 "Start", "Stop" and "Length" descriptors throughout these examples are given in kilo-bases (KB).

The T1-T2 target of the transient connectron 28739 as shown in table 1 is represented as

10

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TP	53531	1	1	4836.528	4836.721	.194	*-*
CPT	53532	1	1	4836.728	4836.746	.019	OS->
TP	53533	1	1	4836.728	4836.746	.019	*-+
15 TN	53534	1	1	4836.728	4836.779	.052	*-+
CPT	53535	1	1	4836.748	4836.779	.032	OS->
TP	53536	1	1	4836.748	4836.779	.032	*-+
CPT	53537	1	1	4836.781	4836.821	.041	OS->
TP	53538	1	1	4836.781	4836.821	.041	*-+
20 TN	53539	1	1	4836.781	4836.918	.138	*-+
TP	53540	1	1	4836.840	4836.855	.016	*-+
CPT	53541	1	1	4836.877	4836.918	.042	OS->
TP	53542	1	1	4836.877	4836.918	.042	*-+
TP	53543	1	1	4836.940	4836.957	.018	*-+
25 CPT	53544	1	1	4836.940	4836.982	.043	OS->
CPT	53545	1	1	4836.990	4837.123	.134	OS->
TP	53546	1	1	4836.990	4837.123	.134	*-+
TN	53547	1	1	4836.990	4837.153	.164	*-+
CPT	53548	1	1	4837.126	4837.148	.023	-->
30 TP	53549	1	1	4837.129	4837.153	.025	*-+
TP	53549a	1	1	4838.155	4838.323	.169	*-*

The "Type" descriptor of the T1 (Id number 53531) is "TP" showing that is T1 target is on the positive strand of the
35 double-stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 53549a) also has the type descriptor "TP".

The T1-T2 loop diagram above can be read by tracing the path from the * of the T1 to the right to the appropriate *, then by tracing a path down the diagram to the first *, then by tracing a path left to the * of the T2. When horizontal lines (indicated by -) intersect with other vertical lines (indicated by |) then the symbol at that point is changed to a +. When the T1-T2 loop does not contain an groups of genes then the vertical symbol (indicated by | or +) is changed to @ as shown below

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
TN	xx	1	1	278.386	279.148	.763	*---*
XX	xx	1	1	278.387	278.416	.030	* @
XX	xx	1	1	278.421	278.450	.030	* @
TP	xx	1	1	278.452	278.892	.441	*---*

Since this synthetic connectron is a virtual connectron there are no gene groups that are controlled by the existence of this connectron. Instead the expression of the C1/C2 sources of six one-shot connectrons (type designator "CPT" for Id numbers 53532, 53535, 53537, 53541, 53544, and 53544) and one transient connectron (type designator "CPT" for Id numbers 53548) are controlled by this connectron.

All of the data for the transient connectron 28739 are pulled together in the following table that is the "terse" description of the connectron.

```

-----
30  Connectron Relationships - Global_Id  Type
                                28739  transient

Control Sequences - Direction  Chromosome  C1/C2_Id      Start      Stop  Length
                                positive      1      . 53464    4832.718  4832.838    .121
35  Trigger Gene - Name        COG_Id      Start      Stop  Length
                                pctC        COG0840  4831.371  4833.269    1.899

```

Target Sequences	- Direction	Chromosome	T1_Id	Start	Stop	Length
	positive	1	53531	4836.528	4836.721	.194

5

T2_Id	Start	Stop	Length
53549a	4838.155	4838.323	.169

Controlled Genes
none

10

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	53532	positive	4836.728	4836.746	.019
2	1	53535	positive	4836.748	4836.779	.032
3	1	53537	positive	4836.781	4836.821	.041
4	1	53541	positive	4836.877	4836.918	.042
5	1	53544	positive	4836.940	4836.982	.043
6	1	53545	positive	4836.990	4837.123	.134
7	1	53548	positive	4837.126	4837.148	.023
8	1	53551	positive	4837.419	4837.448	.030
9	1	53552	positive	4837.572	4837.622	.051
10	1	53554	positive	4837.962	4837.999	.038
11	1	53557	positive	4838.217	4838.258	.042
12	1	53559	positive	4838.295	4838.362	.068
13	1	53563	positive	4838.457	4838.476	.020
14	1	53564	positive	4838.478	4838.645	.168
15	1	53567	positive	4838.654	4838.847	.194

30

The verbose description of the transient connectron 28739 is:

In the *Pseudomonas aeruginosa* PA01, complete genome the transient connectron number 23295 is generated by the control sequence (C1/C2) whose identifier number is 53464. This control sequence is on the positive strand of the genomic DNA of chromosome 1. The genomic start and stop positions of this control sequence are 4832.718 KB and 4832.838 KB with a length of 0.121 KB. Expression of the RNA for this connectron is triggered by the promotion of the gene whose name is pctC and whose COG (Cluster of Orthologous Genes) identifier is COG0840. The genomic start and stop positions of this gene are 4831.371

KB and 4833.269 KB and with a length of 1.899 KB. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the positive strand of the genomic DNA on chromosome 1. The identifier number of the initiating target sequence (T1) is 53531. The genomic start and stop positions of this initiating target sequence are 4836.528 KB and 4836.721 KB with a length of 0.194 KB. The identifier number of the terminating target sequence (T2) is 53569. The genomic start and stop positions of this terminating target sequence are 4838.155 KB and 4838.323 KB with a length of 0.169 KB.

This connectron controls the modulation of the expression of the following gene(s): none

15 This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 53532 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.728 KB and 4836.746 KB with a length of 0.019 KB. (2) The connectron that has the identifier 53535 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.748 KB and 4836.779 KB with a length of 0.032 KB. (3) The connectron that has the identifier 53537 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.781 KB and 4836.821 KB with a length of 0.041 KB. (4) The connectron that has the identifier 53541 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.877 KB and 4836.918 KB with a length of 0.042 KB. (5) The connectron that has the identifier 53544 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.940 KB and 4836.982 KB with a length of

0.043 KB. (6) The connectron that has the identifier 53545 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4836.990 KB and 4837.123 KB with a length of 0.134 KB. (7) The connectron that has the identifier 53548 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4837.126 KB and 4837.148 KB with a length of 0.023 KB. (8) The connectron that has the identifier 53551 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4837.419 KB and 4837.448 KB with a length of 0.030 KB. (9) The connectron that has the identifier 53552 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4837.572 KB and 4837.622 KB with a length of 0.051 KB. (10) The connectron that has the identifier 53554 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4837.962 KB and 4837.999 KB with a length of 0.038 KB. (11) The connectron that has the identifier 53557 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4838.217 KB and 4838.258 KB with a length of 0.042 KB. (12) The connectron that has the identifier 53559 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4838.295 KB and 4838.362 KB with a length of 0.068 KB. (13) The connectron that has the identifier 53563 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4838.457 KB and 4838.476 KB with a length of 0.020 KB. (14) The connectron that has the identifier 53564 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 4838.478 KB and 4838.645 KB with a length of 0.168 KB. (15) The connectron that has the identifier 53567 is on chromosome 1 in the positive direction. The genomic start and

5	GG	620	1	1	954.684	958.635	3.951	Group0128					
	GP	621	1	1	955.956	956.342	.387	VC0897					
	CPT	622	1	1	956.873	956.887	.015	-->					
	CPT	623	1	1	956.896	956.910	.015	-->					
	TN	624	1	1	958.089	958.103	.015	*-+*					
10	GG	625	1	1	958.840	972.992	14.152	Group0129					
	GP	626	1	1	971.304	972.992	1.689	VC0911					
	TP	627	1	1	973.170	973.250	.081	*-+*					
	GG	628	1	1	973.171	973.763	.592	Group0130					
	CPT	629	1	1	973.339	973.434	.096	OS->					
15	CPT	630	1	1	973.508	973.603	.096	OS->					
	TP	631	1	1	973.693	973.773	.081	*-+*					
	GG	632	1	1	973.767	996.501	22.734	Group0131					
	GP	633	1	1	974.049	978.217	4.169	VC0913					
	CPT	634	1	1	977.711	977.725	.015	-->					
20	CPT	635	1	1	977.732	977.746	.015	-->					
	GP	636	1	1	986.166	990.921	4.756	VC0923					
	CPT	637	1	1	986.862	986.877	.016	-->					
	CPT	638	1	1	986.885	986.899	.015	-->					
	TN	639	1	1	996.556	996.577	.022	*-+**					
25	TP	640	1	1	996.556	996.577	.022	*-++-+++++					
	GG	641	1	1	996.656	1005.792	9.136	Group0132					
	GP	642	1	1	1002.462	1005.792	3.331	VC0937					
	TP	643	1	1	1005.810	1005.874	.065	*-+++++					
	CNT	644	1	1	1005.810	1005.921	.112	OS->					
	CPT	645	1	1	1005.810	1005.926	.117	-->					
	TN	646	1	1	1005.810	1005.926	.117	*-+++++					

Group0127 through Group0132 are described in Table 2 as

30

Group0127

35

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
VC0894	COG0607	P	1	positive	952.846	954.393	1.548

Group0128

40

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
VC0895		1	negative	954.684	954.860	.177	
VC0896	COG0583	K	1	positive	955.014	955.934	.921
VC0897	COG2363	S	1	positive	955.956	956.342	.387
VC0898	COG0258	L	1	negative	956.372	957.223	.852
VC0899	COG1611	R	1	negative	957.262	958.635	1.374

45

Group0129

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	VC0900	COG2199	T	1 negative	958.840	960.414	1.575
	VC0901	COG0457	R	1 negative	960.516	962.777	2.262
5	VC0902	COG0780	R	1 negative	962.792	963.655	.864
	VC0903			1 positive	963.686	964.282	.597
	VC0904			1 positive	964.284	965.060	.777
	VC0905	COG1464	M	1 negative	965.193	966.020	.828
	VC0906	COG2011	R	1 negative	966.039	967.740	1.702
	VC0908	COG0241	E	1 positive	967.976	968.536	.561
10	VC0909	COG1609	K	1 positive	968.601	969.551	.951
	VC0910	COG1263	G	1 positive	969.788	971.224	1.437
	VC0911	COG0366	G	1 positive	971.304	972.992	1.689

15	Group0130						
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	tRNA-Tyr-2			1 positive	973.171	973.255	.085
	tRNA-Tyr-3			1 positive	973.340	973.424	.085
20	tRNA-Tyr-4			1 positive	973.509	973.593	.085
	tRNA-Tyr-5			1 positive	973.679	973.763	.085

	Group0131						
25	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
	VC0912			1 positive	973.767	973.862	.096
	VC0913	COG0845	Q	1 positive	974.049	978.217	4.169
	VC0915			1 positive	978.272	978.382	.111
	VC0916	COG0394	T	1 positive	978.644	979.144	.501
	VC0917	COG0381	M	1 positive	979.457	980.575	1.119
30	VC0918	COG0677	M	1 positive	980.595	986.155	5.561
	VC0923	COG1045	E	1 positive	986.166	990.921	4.756
	VC0928			1 positive	991.117	991.932	.816
	VC0929			1 negative	992.138	993.364	1.227
	VC0930			1 positive	993.628	996.501	2.874
35	-----						
	Group0132						
	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
40	VC0931	COG3307	M	1 negative	996.656	997.972	1.317
	VC0932			1 negative	998.148	998.752	.605
	VC0934	COG2148	M	1 positive	999.242	1000.639	1.398
	VC0935			1 positive	1000.710	1001.906	1.197
	VC0936	COG1596	M	1 positive	1001.910	1002.437	.528
45	VC0937	COG3206	N	1 positive	1002.462	1005.792	3.331

All of the data for the transient connectron 7580 are pulled together in the following table that is the "terse" description of the connectron.

5

Connectron Relationships - Global_Id Type
7580 synthetic

10

Control Sequences - Synthetic DNA Binding Protein that recognizes the sequence
tccccatgag catagatatg caggtaggcg gcaagt

Target Sequences - Direction Chromosome T1_Id Start Stop Length
negative 1 607 952.777 952.642 .136

15

T2_Id Start Stop Length
646 1005.926 1005.810 .117

Controlled Genes

20

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0127	VC0894	COG0607	positive	952.846	954.393	1.548
2	1	Group0128	VC0895		positive	954.684	958.635	3.951
3	1	Group0128	VC0896	COG0583	positive	955.014	955.934	.921
4	1	Group0128	VC0897	COG2363	positive	955.956	956.342	.387
5	1	Group0128	VC0898	COG0258	negative	957.223	956.372	.852
6	1	Group0128	VC0899	COG1611	negative	958.635	957.262	1.374
7	1	Group0129	VC0900	COG2199	positive	958.840	972.992	14.152
8	1	Group0129	VC0901	COG0457	negative	962.777	960.516	2.262
9	1	Group0129	VC0902	COG0780	negative	963.655	962.792	.864
10	1	Group0129	VC0903		positive	963.686	964.282	.597
11	1	Group0129	VC0904		positive	964.284	965.060	.777
12	1	Group0129	VC0905	COG1464	negative	966.020	965.193	.828
13	1	Group0129	VC0906	COG2011	negative	967.740	966.039	1.702
14	1	Group0129	VC0908	COG0241	positive	967.976	968.536	.561
15	1	Group0129	VC0909	COG1609	positive	968.601	969.551	.951
16	1	Group0129	VC0910	COG1263	positive	969.788	971.224	1.437
17	1	Group0129	VC0911	COG0366	positive	971.304	972.992	1.689
18	1	Group0130	tRNA-Tyr-		positive	973.171	973.763	.592
19	1	Group0131	VC0912		positive	973.767	996.501	22.734
20	1	Group0131	VC0913	COG0845	positive	974.049	978.217	4.169
21	1	Group0131	VC0915		positive	978.272	978.382	.111
22	1	Group0131	VC0916	COG0394	positive	978.644	979.144	.501
23	1	Group0131	VC0917	COG0381	positive	979.457	980.575	1.119
24	1	Group0131	VC0918	COG0677	positive	980.595	986.155	5.561
25	1	Group0131	VC0923	COG1045	positive	986.166	990.921	4.756
26	1	Group0131	VC0928		positive	991.117	991.932	.816

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5	27	1	Group0131	VC0929	negative	993.364	992.138	1.227
	28	1	Group0131	VC0930	positive	993.628	996.501	2.874
	29	1	Group0132	VC0931	COG3307 positive	996.656	1005.792	9.136
	30	1	Group0132	VC0932	negative	998.752	998.148	.605
	31	1	Group0132	VC0934	COG2148 positive	999.242	1000.639	1.398
	32	1	Group0132	VC0935	positive	1000.710	1001.906	1.197
	33	1	Group0132	VC0936	COG1596 positive	1001.910	1002.437	.528
	34	1	Group0132	VC0937	COG3206 positive	1002.462	1005.792	3.331

10 Controlled Connectrons

	Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
15	1	1	612	negative	954.589	954.497	.093
	2	1	613	positive	954.503	954.520	.018
	3	1	614	positive	954.522	954.588	.067
	4	1	617	negative	954.658	954.616	.043
	5	1	618	positive	954.624	954.639	.016
	6	1	619	positive	954.641	954.658	.018
	7	1	622	positive	956.873	956.887	.015
	8	1	623	positive	956.896	956.910	.015
20	9	1	629	positive	973.339	973.434	.096
	10	1	630	positive	973.508	973.603	.096
	11	1	634	positive	977.711	977.725	.015
	12	1	635	positive	977.732	977.746	.015
25	13	1	637	positive	986.862	986.877	.016
	14	1	638	positive	986.885	986.899	.015
	15	1	644	negative	1005.921	1005.810	.112
	16	1	645	positive	1005.810	1005.926	.117

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The verbose description of the synthetic connectron 7580 is:

In the *Vibrio cholerae* chromosome I, complete chromosome the synthetic connectron number 7580 is generated by a synthetic DNA binding protein that recognizes the sequence

tccccatgagcatagatatgcaggtaggcggcaagt. This connectron causes stabilization of a loop of DNA. The target sequences (T1-T2) are on the negative strand of the genomic DNA on chromosome 1. The identifier number of the initiating target sequence (T1) is

607. The genomic start and stop positions of this initiating target sequence are 952.777 KB and 952.642 KB with a length of 0.136 KB. The identifier number of the terminating target

sequence (T2) is 646. The genomic start and stop positions of this terminating target sequence are 1005.926 KB and 1005.810 KB with a length of 0.117 KB.

- 5 This connectron controls the modulation of the expression of the following gene(s): (1) The gene that has the name VC0894 and with a COG identifier of COG0607. The genomic start and stop positions of this gene are 952.846 KB and 954.393 KB with a length of 1.548 KB. (2) The gene that has the name VC0895. The
10 genomic start and stop positions of this gene are 954.684 KB and 958.635 KB with a length of 3.951 KB. (3) The gene that has the name VC0896 and with a COG identifier of COG0583. The genomic start and stop positions of this gene are 955.014 KB and 955.934 KB with a length of 0.921 KB. (4) The gene that has the name
15 VC0897 and with a COG identifier of COG2363. The genomic start and stop positions of this gene are 955.956 KB and 956.342 KB with a length of 0.387 KB. (5) The gene that has the name VC0898 and with a COG identifier of COG0258. The genomic start and stop positions of this gene are 957.223 KB and 956.372 KB with a
20 length of 0.852 KB. (6) The gene that has the name VC0899 and with a COG identifier of COG1611. The genomic start and stop positions of this gene are 958.635 KB and 957.262 KB with a length of 1.374 KB. (7) The gene that has the name VC0900 and with a COG identifier of COG2199. The genomic start and stop
25 positions of this gene are 958.840 KB and 972.992 KB with a length of 14.152 KB. (8) The gene that has the name VC0901 and with a COG identifier of COG0457. The genomic start and stop positions of this gene are 962.777 KB and 960.516 KB with a length of 2.262 KB. (9) The gene that has the name VC0902 and
30 with a COG identifier of COG0780. The genomic start and stop positions of this gene are 963.655 KB and 962.792 KB with a length of 0.864 KB. (10) The gene that has the name VC0903. The

genomic start and stop positions of this gene are 963.686 KB and 964.282 KB with a length of 0.597 KB. (11) The gene that has the name VC0904. The genomic start and stop positions of this gene are 964.284 KB and 965.060 KB with a length of 0.777 KB. (12)

5 The gene that has the name VC0905 and with a COG identifier of COG1464. The genomic start and stop positions of this gene are 966.020 KB and 965.193 KB with a length of 0.828 KB. (13) The gene that has the name VC0906 and with a COG identifier of COG2011. The genomic start and stop positions of this gene are

10 967.740 KB and 966.039 KB with a length of 1.702 KB. (14) The gene that has the name VC0908 and with a COG identifier of COG0241. The genomic start and stop positions of this gene are 967.976 KB and 968.536 KB with a length of 0.561 KB. (15) The gene that has the name VC0909 and with a COG identifier of

15 COG1609. The genomic start and stop positions of this gene are 968.601 KB and 969.551 KB with a length of 0.951 KB. (16) The gene that has the name VC0910 and with a COG identifier of COG1263. The genomic start and stop positions of this gene are 969.788 KB and 971.224 KB with a length of 1.437 KB. (17) The

20 gene that has the name VC0911 and with a COG identifier of COG0366. The genomic start and stop positions of this gene are 971.304 KB and 972.992 KB with a length of 1.689 KB. (18) The gene that has the name tRNA-Tyr-. The genomic start and stop positions of this gene are 973.171 KB and 973.763 KB with a

25 length of 0.592 KB. (19) The gene that has the name VC0912. The genomic start and stop positions of this gene are 973.767 KB and 996.501 KB with a length of 22.734 KB. (20) The gene that has the name VC0913 and with a COG identifier of COG0845. The genomic start and stop positions of this gene are 974.049 KB and

30 978.217 KB with a length of 4.169 KB. (21) The gene that has the name VC0915. The genomic start and stop positions of this gene are 978.272 KB and 978.382 KB with a length of 0.111 KB. (22)

The gene that has the name VC0916 and with a COG identifier of COG0394. The genomic start and stop positions of this gene are 978.644 KB and 979.144 KB with a length of 0.501 KB. (23) The gene that has the name VC0917 and with a COG identifier of

5 COG0381. The genomic start and stop positions of this gene are 979.457 KB and 980.575 KB with a length of 1.119 KB. (24) The gene that has the name VC0918 and with a COG identifier of COG0677. The genomic start and stop positions of this gene are 980.595 KB and 986.155 KB with a length of 5.561 KB. (25) The

10 gene that has the name VC0923 and with a COG identifier of COG1045. The genomic start and stop positions of this gene are 986.166 KB and 990.921 KB with a length of 4.756 KB. (26) The gene that has the name VC0928. The genomic start and stop positions of this gene are 991.117 KB and 991.932 KB with a

15 length of 0.816 KB. (27) The gene that has the name VC0929. The genomic start and stop positions of this gene are 993.364 KB and 992.138 KB with a length of 1.227 KB. (28) The gene that has the name VC0930. The genomic start and stop positions of this gene are 993.628 KB and 996.501 KB with a length of 2.874 KB. (29)

20 The gene that has the name VC0931 and with a COG identifier of COG3307. The genomic start and stop positions of this gene are 996.656 KB and 1005.792 KB with a length of 9.136 KB. (30) The gene that has the name VC0932. The genomic start and stop positions of this gene are 998.752 KB and 998.148 KB with a

25 length of 0.605 KB. (31) The gene that has the name VC0934 and with a COG identifier of COG2148. The genomic start and stop positions of this gene are 999.242 KB and 1000.639 KB with a length of 1.398 KB. (32) The gene that has the name VC0935. The genomic start and stop positions of this gene are 1000.710 KB

30 and 1001.906 KB with a length of 1.197 KB. (33) The gene that has the name VC0936 and with a COG identifier of COG1596. The genomic start and stop positions of this gene are 1001.910 KB

and 1002.437 KB with a length of 0.528 KB. (34) The gene that has the name VC0937 and with a COG identifier of COG3206. The genomic start and stop positions of this gene are 1002.462 KB and 1005.792 KB with a length of 3.331 KB.

5

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 612 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 954.589

10 KB and 954.497 KB with a length of 0.093 KB. (2) The connectron that has the identifier 613 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.503 KB and 954.520 KB with a length of 0.018 KB. (3) The connectron that has the identifier 614 is on

15 chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.522 KB and 954.588 KB with a length of 0.067 KB. (4) The connectron that has the identifier 617 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 954.658

20 KB and 954.616 KB with a length of 0.043 KB. (5) The connectron that has the identifier 618 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.624 KB and 954.639 KB with a length of 0.016 KB. (6) The connectron that has the identifier 619 is on

25 chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.641 KB and 954.658 KB with a length of 0.018 KB. (7) The connectron that has the identifier 622 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 956.873

30 KB and 956.887 KB with a length of 0.015 KB. (8) The connectron that has the identifier 623 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

connectron are 956.896 KB and 956.910 KB with a length of 0.015 KB. (9) The connectron that has the identifier 629 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 973.339 KB and 973.434 KB with a length of 0.096 KB. (10) The connectron that has the identifier 630 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 973.508 KB and 973.603 KB with a length of 0.096 KB. (11) The connectron that has the identifier 634 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 977.711 KB and 977.725 KB with a length of 0.015 KB. (12) The connectron that has the identifier 635 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 977.732 KB and 977.746 KB with a length of 0.015 KB. (13) The connectron that has the identifier 637 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 986.862 KB and 986.877 KB with a length of 0.016 KB. (14) The connectron that has the identifier 638 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 986.885 KB and 986.899 KB with a length of 0.015 KB. (15) The connectron that has the identifier 644 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 1005.921 KB and 1005.810 KB with a length of 0.112 KB. (16) The connectron that has the identifier 645 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 1005.810 KB and 1005.926 KB with a length of 0.117 KB.

30

Synthetic Connectron formed by a PNA

A synthetic connectron can be introduced into the *V. cholerae* genome by introducing a PNA that recognizes the sequence

5 tccccatgag catagatatg caggtaggcg gcaagt

Connectron 7581 is an example of a synthetic transient connectron.

10

		C1/C2		T1-T2			
Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
7581	1	Synthetic PNA		1	607	646	synthetic

The T1-T2 target of the transient connectron 7581 as shown in
15 Table 1 is represented as

20

Type	Num	Jobno	Chr	Start	Stop	Length	GeneName	
TN	607	1	1	952.642	952.777	.136		*-+++++*****
TP	608	1	1	952.648	952.777	.130		*-++++~+++~*++++*~+++++~++++
GG	609	1	1	952.846	954.393	1.548	Group0127	
TN	610	1	1	954.486	954.587	.102		*-+++++*****-+++-+*~+++++*
TP	611	1	1	954.486	954.587	.102		*-+++++*****+*****~*~++-++*~
CNT	612	1	1	954.497	954.589	.093	OS->	
CPT	613	1	1	954.503	954.520	.018	-->	
CPT	614	1	1	954.522	954.588	.067	-->	
TP	615	1	1	954.601	954.658	.058		*-+++++*****+*****+*~++-+*
TN	616	1	1	954.602	954.658	.057		*-+++++*****+*****+*~
CNT	617	1	1	954.616	954.658	.043	-->	
CPT	618	1	1	954.624	954.639	.016	-->	
CPT	619	1	1	954.641	954.658	.018	-->	
GG	620	1	1	954.684	958.635	3.951	Group0128	
GP	621	1	1	955.956	956.342	.387	VC0897	
CPT	622	1	1	956.873	956.887	.015	-->	
CPT	623	1	1	956.896	956.910	.015	-->	
TN	624	1	1	958.089	958.103	.015		*~+*
GG	625	1	1	958.840	972.992	14.152	Group0129	_
GP	626	1	1	971.304	972.992	1.689	VC0911	
TP	627	1	1	973.170	973.250	.081		*~+*
GG	628	1	1	973.171	973.763	.592	Group0130	
CPT	629	1	1	973.339	973.434	.096	OS->	
CPT	630	1	1	973.508	973.603	.096	OS->	
TP	631	1	1	973.693	973.773	.081		*~+*

5	GG	632	1	1	973.767	996.501	22.734	Group0131	
	GP	633	1	1	974.049	978.217	4.169	VC0913	
	CPT	634	1	1	977.711	977.725	.015	-->	
	CPT	635	1	1	977.732	977.746	.015	-->	
	GP	636	1	1	986.166	990.921	4.756	VC0923	
10	CPT	637	1	1	986.862	986.877	.016	-->	
	CPT	638	1	1	986.885	986.899	.015	-->	
	TN	639	1	1	996.556	996.577	.022	*-+**	
	TP	640	1	1	996.556	996.577	.022	*-+-+*****	
	GG	641	1	1	996.656	1005.792	9.136	Group0132	
15	GP	642	1	1	1002.462	1005.792	3.331	VC0937	
	TP	643	1	1	1005.810	1005.874	.065	*-+*****	
	CNT	644	1	1	1005.810	1005.921	.112	OS->	
	CPT	645	1	1	1005.810	1005.926	.117	-->	
	TN	646	1	1	1005.810	1005.926	.117	*-+*****	

Group0127 through Group0132 are described in Table 2 as

20 Group0127

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
VC0894	COG0607	P	1	positive	952.846	954.393	1.548

25 Group0128

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
VC0895		1	negative	954.684	954.860	.177	
VC0896	COG0583	K	1	positive	955.014	955.934	.921
VC0897	COG2363	S	1	positive	955.956	956.342	.387
VC0898	COG0258	L	1	negative	956.372	957.223	.852
VC0899	COG1611	R	1	negative	957.262	958.635	1.374

35 Group0129

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
VC0900	COG2199	T	1	negative	958.840	960.414	1.575
VC0901	COG0457	R	1	negative	960.516	962.777	2.262
VC0902	COG0780	R	1	negative	962.792	963.655	.864
VC0903			1	positive	963.686	964.282	.597
VC0904			1	positive	964.284	965.060	.777
VC0905	COG1464	M	1	negative	965.193	966.020	.828
VC0906	COG2011	R	1	negative	966.039	967.740	1.702
VC0908	COG0241	E	1	positive	967.976	968.536	.561
VC0909	COG1609	K	1	positive	968.601	969.551	.951
VC0910	COG1263	G	1	positive	969.788	971.224	1.437
VC0911	COG0366	G	1	positive	971.304	972.992	1.689

Group0130

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
5	tRNA-Tyr-2		1	positive	973.171	973.255	.085
	tRNA-Tyr-3		1	positive	973.340	973.424	.085
	tRNA-Tyr-4		1	positive	973.509	973.593	.085
	tRNA-Tyr-5		1	positive	973.679	973.763	.085

10 Group0131

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
15	VC0912		1	positive	973.767	973.862	.096	
	VC0913	COG0845	Q	1	positive	974.049	978.217	4.169
	VC0915		1	positive	978.272	978.382	.111	
	VC0916	COG0394	T	1	positive	978.644	979.144	.501
	VC0917	COG0381	M	1	positive	979.457	980.575	1.119
	VC0918	COG0677	M	1	positive	980.595	986.155	5.561
20	VC0923	COG1045	E	1	positive	986.166	990.921	4.756
	VC0928		1	positive	991.117	991.932	.816	
	VC0929		1	negative	992.138	993.364	1.227	
	VC0930		1	positive	993.628	996.501	2.874	

Group0132

25

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
VC0931	COG3307	M	1	negative	996.656	997.972	1.317
VC0932			1	negative	998.148	998.752	.605
VC0934	COG2148	M	1	positive	999.242	1000.639	1.398
VC0935			1	positive	1000.710	1001.906	1.197
VC0936	COG1596	M	1	positive	1001.910	1002.437	.528
VC0937	COG3206	N	1	positive	1002.462	1005.792	3.331

30

35 All of the data for the transient connectron 7581 are pulled together in the following table that is the "terse" description of the connectron.

40

Connectron Relationships - Global_Id Type
7581 synthetic

45 Control Sequences - Synthetic PNA that recognizes the sequence
tccccatgag catagatatg caggtaggcg gcaagt

Target Sequences	- Direction	Chromosome	T1_Id	Start	Stop	Length
	negative	1	607	952.777	952.642	.136

5

T2_Id	Start	Stop	Length
646	1005.926	1005.810	.117

Controlled Genes

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0127	VC0894	COG0607	positive	952.846	954.393	1.548
2	1	Group0128	VC0895		positive	954.684	958.635	3.951
3	1	Group0128	VC0896	COG0583	positive	955.014	955.934	.921
4	1	Group0128	VC0897	COG2363	positive	955.956	956.342	.387
5	1	Group0128	VC0898	COG0258	negative	957.223	956.372	.852
6	1	Group0128	VC0899	COG1611	negative	958.635	957.262	1.374
7	1	Group0129	VC0900	COG2199	positive	958.840	972.992	14.152
8	1	Group0129	VC0901	COG0457	negative	962.777	960.516	2.262
9	1	Group0129	VC0902	COG0780	negative	963.655	962.792	.864
10	1	Group0129	VC0903		positive	963.686	964.282	.597
11	1	Group0129	VC0904		positive	964.284	965.060	.777
12	1	Group0129	VC0905	COG1464	negative	966.020	965.193	.828
13	1	Group0129	VC0906	COG2011	negative	967.740	966.039	1.702
14	1	Group0129	VC0908	COG0241	positive	967.976	968.536	.561
15	1	Group0129	VC0909	COG1609	positive	968.601	969.551	.951
16	1	Group0129	VC0910	COG1263	positive	969.788	971.224	1.437
17	1	Group0129	VC0911	COG0366	positive	971.304	972.992	1.689
18	1	Group0130	tRNA-Tyr-		positive	973.171	973.763	.592
19	1	Group0131	VC0912		positive	973.767	996.501	22.734
20	1	Group0131	VC0913	COG0845	positive	974.049	978.217	4.169
21	1	Group0131	VC0915		positive	978.272	978.382	.111
22	1	Group0131	VC0916	COG0394	positive	978.644	979.144	.501
23	1	Group0131	VC0917	COG0381	positive	979.457	980.575	1.119
24	1	Group0131	VC0918	COG0677	positive	980.595	986.155	5.561
25	1	Group0131	VC0923	COG1045	positive	986.166	990.921	4.756
26	1	Group0131	VC0928		positive	991.117	991.932	.816
27	1	Group0131	VC0929		negative	993.364	992.138	1.227
28	1	Group0131	VC0930		positive	993.628	996.501	2.874
29	1	Group0132	VC0931	COG3307	positive	996.656	1005.792	9.136
30	1	Group0132	VC0932		negative	998.752	998.148	.605
31	1	Group0132	VC0934	COG2148	positive	999.242	1000.639	1.398
32	1	Group0132	VC0935		positive	1000.710	1001.906	1.197
33	1	Group0132	VC0936	COG1596	positive	1001.910	1002.437	.528
34	1	Group0132	VC0937	COG3206	positive	1002.462	1005.792	3.331

Controlled Connectrons

Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
1	1	612	negative	954.589	954.497	.093
2	1	613	positive	954.503	954.520	.018
3	1	614	positive	954.522	954.588	.067

	4	1	617	negative	954.658	954.616	.043
	5	1	618	positive	954.624	954.639	.016
	6	1	619	positive	954.641	954.658	.018
5	7	1	622	positive	956.873	956.887	.015
	8	1	623	positive	956.896	956.910	.015
	9	1	629	positive	973.339	973.434	.096
	10	1	630	positive	973.508	973.603	.096
	11	1	634	positive	977.711	977.725	.015
10	12	1	635	positive	977.732	977.746	.015
	13	1	637	positive	986.862	986.877	.016
	14	1	638	positive	986.885	986.899	.015
	15	1	644	negative	1005.921	1005.810	.112
	16	1	645	positive	1005.810	1005.926	.117
15	-----						

The verbose description of the synthetic connectron 7581 is:

In the *Vibrio cholerae* chromosome I, complete chromosome the
 20 synthetic connectron number 7580 is generated by a synthetic PNA
 that recognizes the sequence
 tccccatgagcatagatatgcaggtaggcggcaagt. This connectron causes
 stabilization of a loop of DNA. The target sequences (T1-T2)
 are on the negative strand of the genomic DNA on chromosome 1.
 25 The identifier number of the initiating target sequence (T1) is
 607. The genomic start and stop positions of this initiating
 target sequence are 952.777 KB and 952.642 KB with a length of
 0.136 KB. The identifier number of the terminating target
 sequence (T2) is 646. The genomic start and stop positions of
 30 this terminating target sequence are 1005.926 KB and 1005.810 KB
 with a length of 0.117 KB.

This connectron controls the modulation of the expression of the
 following gene(s): (1) The gene that has the name VC0894 and
 35 with a COG identifier of COG0607. The genomic start and stop
 positions of this gene are 952.846 KB and 954.393 KB with a
 length of 1.548 KB. (2) The gene that has the name VC0895. The

genomic start and stop positions of this gene are 954.684 KB and 958.635 KB with a length of 3.951 KB. (3) The gene that has the name VC0896 and with a COG identifier of COG0583. The genomic start and stop positions of this gene are 955.014 KB and 955.934

5 KB with a length of 0.921 KB. (4) The gene that has the name VC0897 and with a COG identifier of COG2363. The genomic start and stop positions of this gene are 955.956 KB and 956.342 KB with a length of 0.387 KB. (5) The gene that has the name VC0898 and with a COG identifier of COG0258. The genomic start and

10 stop positions of this gene are 957.223 KB and 956.372 KB with a length of 0.852 KB. (6) The gene that has the name VC0899 and with a COG identifier of COG1611. The genomic start and stop positions of this gene are 958.635 KB and 957.262 KB with a length of 1.374 KB. (7) The gene that has the name VC0900 and

15 with a COG identifier of COG2199. The genomic start and stop positions of this gene are 958.840 KB and 972.992 KB with a length of 14.152 KB. (8) The gene that has the name VC0901 and with a COG identifier of COG0457. The genomic start and stop positions of this gene are 962.777 KB and 960.516 KB with a

20 length of 2.262 KB. (9) The gene that has the name VC0902 and with a COG identifier of COG0780. The genomic start and stop positions of this gene are 963.655 KB and 962.792 KB with a length of 0.864 KB. (10) The gene that has the name VC0903. The genomic start and stop positions of this gene are 963.686 KB and

25 964.282 KB with a length of 0.597 KB. (11) The gene that has the name VC0904. The genomic start and stop positions of this gene are 964.284 KB and 965.060 KB with a length of 0.777 KB. (12) The gene that has the name VC0905 and with a COG identifier of COG1464. The genomic start and stop positions of this gene are

30 966.020 KB and 965.193 KB with a length of 0.828 KB. (13) The gene that has the name VC0906 and with a COG identifier of COG2011. The genomic start and stop positions of this gene are

967.740 KB and 966.039 KB with a length of 1.702 KB. (14) The gene that has the name VC0908 and with a COG identifier of COG0241. The genomic start and stop positions of this gene are 967.976 KB and 968.536 KB with a length of 0.561 KB. (15) The

5 gene that has the name VC0909 and with a COG identifier of COG1609. The genomic start and stop positions of this gene are 968.601 KB and 969.551 KB with a length of 0.951 KB. (16) The gene that has the name VC0910 and with a COG identifier of COG1263. The genomic start and stop positions of this gene are

10 969.788 KB and 971.224 KB with a length of 1.437 KB. (17) The gene that has the name VC0911 and with a COG identifier of COG0366. The genomic start and stop positions of this gene are 971.304 KB and 972.992 KB with a length of 1.689 KB. (18) The gene that has the name tRNA-Tyr-. The genomic start and stop

15 positions of this gene are 973.171 KB and 973.763 KB with a length of 0.592 KB. (19) The gene that has the name VC0912. The genomic start and stop positions of this gene are 973.767 KB and 996.501 KB with a length of 22.734 KB. (20) The gene that has the name VC0913 and with a COG identifier of COG0845. The

20 genomic start and stop positions of this gene are 974.049 KB and 978.217 KB with a length of 4.169 KB. (21) The gene that has the name VC0915. The genomic start and stop positions of this gene are 978.272 KB and 978.382 KB with a length of 0.111 KB. (22) The gene that has the name VC0916 and with a COG identifier of

25 COG0394. The genomic start and stop positions of this gene are 978.644 KB and 979.144 KB with a length of 0.501 KB. (23) The gene that has the name VC0917 and with a COG identifier of COG0381. The genomic start and stop positions of this gene are 979.457 KB and 980.575 KB with a length of 1.119 KB. (24) The

30 gene that has the name VC0918 and with a COG identifier of COG0677. The genomic start and stop positions of this gene are 980.595 KB and 986.155 KB with a length of 5.561 KB. (25) The

gene that has the name VC0923 and with a COG identifier of COG1045. The genomic start and stop positions of this gene are 986.166 KB and 990.921 KB with a length of 4.756 KB. (26) The gene that has the name VC0928. The genomic start and stop positions of this gene are 991.117 KB and 991.932 KB with a length of 0.816 KB. (27) The gene that has the name VC0929. The genomic start and stop positions of this gene are 993.364 KB and 992.138 KB with a length of 1.227 KB. (28) The gene that has the name VC0930. The genomic start and stop positions of this gene are 993.628 KB and 996.501 KB with a length of 2.874 KB. (29) The gene that has the name VC0931 and with a COG identifier of COG3307. The genomic start and stop positions of this gene are 996.656 KB and 1005.792 KB with a length of 9.136 KB. (30) The gene that has the name VC0932. The genomic start and stop positions of this gene are 998.752 KB and 998.148 KB with a length of 0.605 KB. (31) The gene that has the name VC0934 and with a COG identifier of COG2148. The genomic start and stop positions of this gene are 999.242 KB and 1000.639 KB with a length of 1.398 KB. (32) The gene that has the name VC0935. The genomic start and stop positions of this gene are 1000.710 KB and 1001.906 KB with a length of 1.197 KB. (33) The gene that has the name VC0936 and with a COG identifier of COG1596. The genomic start and stop positions of this gene are 1001.910 KB and 1002.437 KB with a length of 0.528 KB. (34) The gene that has the name VC0937 and with a COG identifier of COG3206. The genomic start and stop positions of this gene are 1002.462 KB and 1005.792 KB with a length of 3.331 KB.

This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 612 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 954.589

KB and 954.497 KB with a length of 0.093 KB. (2) The connectron that has the identifier 613 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.503 KB and 954.520 KB with a length of 0.018 KB. (3) The connectron that has the identifier 614 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.522 KB and 954.588 KB with a length of 0.067 KB. (4) The connectron that has the identifier 617 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 954.658 KB and 954.616 KB with a length of 0.043 KB. (5) The connectron that has the identifier 618 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.624 KB and 954.639 KB with a length of 0.016 KB. (6) The connectron that has the identifier 619 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 954.641 KB and 954.658 KB with a length of 0.018 KB. (7) The connectron that has the identifier 622 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 956.873 KB and 956.887 KB with a length of 0.015 KB. (8) The connectron that has the identifier 623 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 956.896 KB and 956.910 KB with a length of 0.015 KB. (9) The connectron that has the identifier 629 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 973.339 KB and 973.434 KB with a length of 0.096 KB. (10) The connectron that has the identifier 630 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 973.508 KB and 973.603 KB with a length of 0.096 KB. (11) The connectron that has the identifier 634 is on chromosome 1 in the positive

direction. The genomic start and stop positions of this connectron are 977.711 KB and 977.725 KB with a length of 0.015 KB. (12) The connectron that has the identifier 635 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 977.732 KB and 977.746 KB with a length of 0.015 KB. (13) The connectron that has the identifier 637 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 986.862 KB and 986.877 KB with a length of 0.016 KB. (14) The connectron that has the identifier 638 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 986.885 KB and 986.899 KB with a length of 0.015 KB. (15) The connectron that has the identifier 644 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 1005.921 KB and 1005.810 KB with a length of 0.112 KB. (16) The connectron that has the identifier 645 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 1005.810 KB and 1005.926 KB with a length of 0.117 KB.

20

Synthetic Connectron formed by a Pair of Linked DNA Binding Objects

25

A synthetic connectron can be introduced into the *A. pernix* genome by introducing a pair of linked DNA binding objects that recognize the sequences

30 G1 cccgacacaacctgc
and
G2 cccgggggttcccag

Connectron 917 is an example of a synthetic transient connectron.

5	C1/C2				T1-T2			
	Global_Id	Chromosome	C1_Id	C2_Id	Chromosome	T1_Id	T2_Id	Connectron_Type
	917	1	G1	G2	1	218	295	synthetic

The T1-T2 target of the transient connectron 917 as shown in Table 1 is represented as

10

	Type	Num	Jobno	Chr	Start	Stop	Length	GeneName
	TN	218	1	1	284.008	284.071	.064	*-+++-+++
	TP	219	1	1	284.008	284.071	.064	*-+++*
	CPT	220	1	1	284.009	284.071	.063	-->
15	CNT	221	1	1	284.073	284.144	.072	-->
	CPT	222	1	1	284.073	284.145	.073	-->
	TP	223	1	1	284.073	284.160	.088	*-+++++*****+
	TN	224	1	1	284.073	284.251	.179	*-+++++*****+***
	CNT	225	1	1	284.158	284.251	.094	-->
20	CPT	226	1	1	284.158	284.251	.094	-->
	TP	227	1	1	284.162	284.251	.090	*-+++++*****
	CPT	228	1	1	284.253	284.280	.028	-->
	TN	229	1	1	284.253	284.305	.053	*-+++++*****
	TP	230	1	1	284.253	284.316	.064	*-+++++*****
25	CPT	231	1	1	284.283	284.305	.023	-->
	GG	232	1	1	284.391	287.510	3.120	Group0053
	TN	233	1	1	286.094	286.108	.015	*-+++++*****
	GG	234	1	1	287.521	291.639	4.118	Group0054
	TP	235	1	1	288.611	288.625	.015	*-++++*
30	GG	236	1	1	291.643	295.139	3.496	Group0055
	TP	237	1	1	295.230	295.259	.030	*-++++*
	GG	238	1	1	295.231	295.529	.298	Group0056
	GP	239	1	1	295.342	295.518	.177	APES013
	CPT	240	1	1	295.415	295.444	.030	-->
35	TP	241	1	1	295.417	295.444	.028	*-+++++*****
	GG	242	1	1	295.572	296.676	1.104	Group0057
	TN	243	1	1	296.080	296.095	.016	*-+++++*****
	TN	244	1	1	296.913	296.927	.015	*-+++++*****
	GG	245	1	1	297.071	298.857	1.786	Group0058
40	TP	246	1	1	298.617	298.631	.015	*-+++++*****
	GG	247	1	1	298.856	305.941	7.085	Group0059
	CNT	248	1	1	300.742	300.757	.016	-->
	CNT	249	1	1	300.767	300.781	.015	-->
	GN	250	1	1	301.243	303.153	1.911	APE0428
45	TN	251	1	1	301.733	301.748	.016	*-+++++*****

	GP	252	1	1	305.005	305.611	.607	APE0434		
	CPT	253	1	1	305.334	305.348	.015	-->		
	CPT	254	1	1	305.358	305.372	.015	-->		
	CNT	255	1	1	305.552	305.566	.015	-->		
5	TN	256	1	1	305.562	305.576	.015		*-+++++*	
	CNT	257	1	1	305.568	305.582	.015	-->		
	GG	258	1	1	306.121	308.859	2.738	Group0060		
	TP	259	1	1	307.532	307.547	.016		*-+++++	
	TN	260	1	1	307.814	307.828	.015		*-+++++	
10	TN	261	1	1	308.559	308.573	.015		*-+++++	
	GG	262	1	1	308.989	312.190	3.201	Group0061		
	TN	263	1	1	311.735	311.750	.016		*-+++++	
	GG	264	1	1	312.215	313.258	1.043	Group0062		
	TP	265	1	1	312.894	312.909	.016		*-+++++	
15	GG	266	1	1	313.378	315.728	2.350	Group0063		
	TN	267	1	1	314.051	314.065	.015		*-+++++	
	TN	268	1	1	314.826	314.840	.015		*-+++++	
	TN	269	1	1	315.511	315.525	.015		*-+++++	
	TP	270	1	1	315.747	315.761	.015		*-+++++	
20	GG	271	1	1	315.792	318.996	3.204	Group0064		
	GP	272	1	1	317.638	318.996	1.359	APE0457		
	CNT	273	1	1	317.668	317.682	.015	-->		
	TP	274	1	1	317.689	317.703	.015		*-+++++	
	CNT	275	1	1	317.690	317.704	.015	-->		
25	GG	276	1	1	318.432	318.914	.483	Group0065		
	CPT	277	1	1	319.097	319.127	.031	-->		
	TN	278	1	1	319.122	319.137	.016		*-+++++	
	GG	279	1	1	319.335	319.673	.339	Group0066		
	TN	280	1	1	319.515	319.529	.015		*-+++++	
30	TP	281	1	1	319.572	319.586	.015		*-+++++	
	GG	282	1	1	319.733	324.526	4.793	Group0067		
	CNT	283	1	1	320.484	320.513	.030	-->		
	GN	284	1	1	320.700	322.241	1.542	APE0462		
	TN	285	1	1	323.674	323.688	.015		*-+++++	
35	GG	286	1	1	324.030	324.335	.306	Group0068		
	TN	287	1	1	324.137	324.151	.015		*-+++++	
	GG	288	1	1	324.606	325.575	.969	Group0069		
	GP	289	1	1	325.141	325.575	.435	APE0469		
	CNT	290	1	1	325.950	325.979	.030	-->		
40	CPT	291	1	1	325.950	325.979	.030	-->		
	TN	292	1	1	325.959	325.975	.017		*-+++++	
	GG	293	1	1	325.980	326.717	.738	Group0070		
	CNT	294	1	1	326.716	326.878	.163	OS->		
	TN	295	1	1	326.716	326.878	.163		*-+++++	

The "Type" descriptor of the T1 (Id number 218) is "TN" showing that is T1 target is on the negative strand of the double-

stranded genomic DNA. Because the T1 and the T2 targets have to be on the same strand, the T2 target (Id number 295) also has the type descriptor "TN".

5 Group0053 through Group0070 are described in Table 2 as

Group0053

10

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0413	COG0553	K	1 negative	284.391	287.510	3.120

Group0054

15

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0414			1 negative	287.521	288.066	.546
APE0415	COG1483	R	1 negative	288.073	291.639	3.567

Group0055

20

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0416	COG1743	L	1 negative	291.643	294.666	3.024
APE0417			1 positive	292.319	292.636	.318
APE0418			1 positive	294.690	295.139	.450

25

Group0056

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
tRNA-Thr			1 positive	295.231	295.325	.095
APES013			1 positive	295.342	295.518	.177
tRNA-Met			1 positive	295.405	295.529	.125

Group0057

35

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APES014			1 negative	295.572	295.754	.183
APE0419			1 negative	295.891	296.676	.786

Group0058

40

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0420			1 positive	297.071	298.113	1.043
APE0422			1 negative	297.448	297.993	.546
APE0423	COG0084	L	1 negative	298.099	298.857	.759

45

Group0059

	Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
5	APE0424			1	positive	298.856	299.269	.414
	APE0425			1	negative	298.973	299.332	.360
	APE0426	COG2246	S	1	positive	299.481	300.602	1.122
	APE0427	COG1573	L	1	positive	300.649	301.296	.648
	APE0428	COG1750	R	1	negative	301.243	303.153	1.911
10	APE0429			1	positive	303.244	303.786	.543
	APE0430			1	negative	303.403	303.720	.318
	APE0431			1	positive	303.833	304.911	1.079
	APE0432			1	negative	304.284	304.688	.405
	APE0434			1	positive	305.005	305.611	.607
	APE0436	COG1093	J	1	negative	305.192	305.941	.750

Group0060

	Gene_Name	COG_Id		Chromosome	Direction	Start	Stop	Length
20	APES015	COG2051	J	1	negative	306.121	306.342	.222
	APES016	COG1631	J	1	negative	306.359	306.550	.192
	APE0437			1	negative	306.674	308.859	2.186
	APE0439			1	positive	307.209	307.841	.633

Group0061

25

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length		
APES017		1	negative	308.989	309.186	.198		
APE0442	COG1594	K	1	negative	309.201	309.515	.315	
APES018		1	negative	309.642	309.842	.201		
30	APE0443	COG1761	K	1	negative	309.915	310.223	.309
	APE0444	COG3286	S	1	negative	310.227	310.832	.606
	APE0445	COG1096	J	1	negative	310.912	312.190	1.279

Group0062

35

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
APE0447	COG1736	J	1	negative	312.215	313.237	1.023
APE0448			1	positive	312.650	313.258	.609

40 Group0063

	Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
45	APE0449	COG0197	J	1	negative	313.378	313.902	.525
	APE0450	COG0303	H	1	positive	313.995	315.728	1.734
	APE0451			1	negative	314.028	314.714	.687

Group0064

5

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
APES019		1	negative	315.792	315.986	.195	
APE0452		1	negative	316.237	316.791	.555	
APE0453		1	positive	316.247	317.576	1.330	
APE0454	COG1489	G	1	negative	316.820	317.542	.723
APE0456		1	negative	317.632	318.099	.468	
APE0457	COG0160	E	1	positive	317.638	318.996	1.359

Group0065							

10

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0458		1	negative	318.432	318.914	.483

Group0066						

15

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0459		1	negative	319.335	319.673	.339

Group0067						

20

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
APE0460		1	positive	319.733	320.038	.306	
APE0461	COG1591	L	1	positive	320.272	320.703	.432
APE0462	COG1855	R	1	negative	320.700	322.241	1.542
APE0463		1	positive	321.610	322.074	.465	
APE0464		1	positive	322.317	323.228	.912	
APE0465	COG0301	H	1	negative	323.288	324.526	1.239

Group0068							

30

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length
APE0466		1	positive	324.030	324.335	.306

Group0069						

35

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
APE0468		1	positive	324.606	325.049	.444	
APE0469	COG1318	K	1	positive	325.141	325.575	.435

Group0070							

40

Gene_Name	COG_Id	Chromosome	Direction	Start	Stop	Length	
APE0470	COG1277	R	1	negative	325.980	326.717	.738

45

All of the data for the transient connectron 917 are pulled together in the following table that is the "terse" description of the connectron.

5

Connectron Relationships - Global_Id Type
917 synthetic

10

Control Sequences - Synthetic Pair of Linked DNA Binding Objects that recognize the sequences G1 = cccgacacaacctgc and G2 = cccgggggttcccgag

Target Sequences	- Direction	Chromosome	T1_Id	Start	Stop	Length
	negative	1	218	284.071	284.008	.064

15

T2_Id	Start	Stop	Length
295	326.878	326.716	.163

Controlled Genes

20

Local_Id	Chromosome	Group	Name	COG_Id	Direction	Start	Stop	Length
1	1	Group0053	APE0413	COG0553	positive	284.391	287.510	3.120
2	1	Group0054	APE0414		positive	287.521	291.639	4.118
3	1	Group0054	APE0415	COG1483	negative	291.639	288.073	3.567
4	1	Group0055	APE0416	COG1743	positive	291.643	295.139	3.496
5	1	Group0055	APE0417		positive	292.319	292.636	.318
6	1	Group0055	APE0418		positive	294.690	295.139	.450
7	1	Group0056	tRNA-Thr		positive	295.231	295.529	.298
8	1	Group0056	APES013		positive	295.342	295.518	.177
9	1	Group0057	APES014		positive	295.572	296.676	1.104
10	1	Group0057	APE0419		negative	296.676	295.891	.786
11	1	Group0058	APE0420		positive	297.071	298.857	1.786
12	1	Group0058	APE0422		negative	297.993	297.448	.546
13	1	Group0058	APE0423	COG0084	negative	298.857	298.099	.759
14	1	Group0059	APE0424		positive	298.856	305.941	7.085
15	1	Group0059	APE0425		negative	299.332	298.973	.360
16	1	Group0059	APE0426	COG2246	positive	299.481	300.602	1.122
17	1	Group0059	APE0427	COG1573	positive	300.649	301.296	.648
18	1	Group0059	APE0428	COG1750	negative	303.153	301.243	1.911
19	1	Group0059	APE0429		positive	303.244	303.786	.543
20	1	Group0059	APE0430		negative	303.720	303.403	.318
21	1	Group0059	APE0431		positive	303.833	304.911	1.079
22	1	Group0059	APE0432		negative	304.688	304.284	.405
23	1	Group0059	APE0434		positive	305.005	305.611	.607
24	1	Group0059	APE0436	COG1093	negative	305.941	305.192	.750
25	1	Group0060	APES015	COG2051	positive	306.121	308.859	2.738
26	1	Group0060	APES016	COG1631	negative	306.550	306.359	.192

5	27	1	Group0060	APE0437	negative	308.859	306.674	2.186
	28	1	Group0060	APE0439	positive	307.209	307.841	.633
	29	1	Group0061	APE0417	positive	308.989	312.190	3.201
	30	1	Group0061	APE0442	COG1594 negative	309.515	309.201	.315
	31	1	Group0061	APE0418	negative	309.842	309.642	.201
10	32	1	Group0061	APE0443	COG1761 negative	310.223	309.915	.309
	33	1	Group0061	APE0444	COG3286 negative	310.832	310.227	.606
	34	1	Group0061	APE0445	COG1096 negative	312.190	310.912	1.279
	35	1	Group0062	APE0447	COG1736 positive	312.215	313.258	1.043
	36	1	Group0062	APE0448	positive	312.650	313.258	.609
15	37	1	Group0063	APE0449	COG0197 positive	313.378	315.728	2.350
	38	1	Group0063	APE0450	COG0303 positive	313.995	315.728	1.734
	39	1	Group0063	APE0451	negative	314.714	314.028	.687
	40	1	Group0064	APE0419	positive	315.792	318.996	3.204
	41	1	Group0064	APE0452	negative	316.791	316.237	.555
20	42	1	Group0064	APE0453	positive	316.247	317.576	1.330
	43	1	Group0064	APE0454	COG1489 negative	317.542	316.820	.723
	44	1	Group0064	APE0456	negative	318.099	317.632	.468
	45	1	Group0064	APE0457	COG0160 positive	317.638	318.996	1.359
	46	1	Group0065	APE0458	positive	318.432	318.914	.483
25	47	1	Group0066	APE0459	positive	319.335	319.673	.339
	48	1	Group0067	APE0460	positive	319.733	324.526	4.793
	49	1	Group0067	APE0461	COG1591 positive	320.272	320.703	.432
	50	1	Group0067	APE0462	COG1855 negative	322.241	320.700	1.542
	51	1	Group0067	APE0463	positive	321.610	322.074	.465
30	52	1	Group0067	APE0464	positive	322.317	323.228	.912
	53	1	Group0067	APE0465	COG0301 negative	324.526	323.288	1.239
	54	1	Group0068	APE0466	positive	324.030	324.335	.306
	55	1	Group0069	APE0468	positive	324.606	325.575	.969
	56	1	Group0069	APE0469	COG1318 positive	325.141	325.575	.435
	57	1	Group0070	APE0470	COG1277 positive	325.980	326.717	.738

Controlled Connectrons

	Local_Id	Chromosome	C1/C2_Id	Direction	Start	Stop	Length
35	1	1	220	positive	284.009	284.071	.063
	2	1	221	negative	284.144	284.073	.072
	3	1	222	positive	284.073	284.145	.073
	4	1	225	negative	284.251	284.158	.094
	5	1	226	positive	284.158	284.251	.094
40	6	1	228	positive	284.253	284.280	.028
	7	1	231	positive	284.283	284.305	.023
	8	1	240	positive	295.415	295.444	.030
	9	1	248	negative	300.757	300.742	.016
	10	1	249	negative	300.781	300.767	.015
45	11	1	253	positive	305.334	305.348	.015
	12	1	254	positive	305.358	305.372	.015
	13	1	255	negative	305.566	305.552	.015
	14	1	257	negative	305.582	305.568	.015

15	1	273	negative	317.682	317.668	.015
16	1	275	negative	317.704	317.690	.015
17	1	277	positive	319.097	319.127	.031
18	1	283	negative	320.513	320.484	.030
5 19	1	290	negative	325.979	325.950	.030
20	1	291	positive	325.950	325.979	.030
21	1	294	negative	326.878	326.716	.163

10

The verbose description of the transient connectron 917 is:

In the *Aeropyrum pernix* K1 complete genome the synthetic connectron number 917 is generated by a synthetic pair of linked
15 DNA binding objects that recognizes the sequences G1 =
cccgacacaacctgc and G2 = cccgggggttcccgag. The target sequences
(T1-T2) are on the negative strand of the genomic DNA on
chromosome 1. The identifier number of the initiating target
sequence (T1) is 218. The genomic start and stop positions of
20 this initiating target sequence are 284.071 KB and 284.008 KB
with a length of 0.064 KB. The identifier number of the
terminating target sequence (T2) is 295. The genomic start and
stop positions of this terminating target sequence are 326.878
KB and 326.716 KB with a length of 0.163 KB.

25

This connectron controls the modulation of the expression of the
following gene(s): (1) The gene that has the name APE0413 and
with a COG identifier of COG0553. The genomic start and stop
positions of this gene are 284.391 KB and 287.510 KB with a
30 length of 3.120 KB. (2) The gene that has the name APE0414. The
genomic start and stop positions of this gene are 287.521 KB and
291.639 KB with a length of 4.118 KB. (3) The gene that has the
name APE0415 and with a COG identifier of COG1483. The genomic
start and stop positions of this gene are 291.639 KB and 288.073
35 KB with a length of 3.567 KB. (4) The gene that has the name

APE0416 and with a COG identifier of COG1743. The genomic start and stop positions of this gene are 291.643 KB and 295.139 KB with a length of 3.496 KB. (5) The gene that has the name APE0417. The genomic start and stop positions of this gene are 292.319 KB and 292.636 KB with a length of 0.318 KB. (6) The gene that has the name APE0418. The genomic start and stop positions of this gene are 294.690 KB and 295.139 KB with a length of 0.450 KB. (7) The gene that has the name tRNA-Thr. The genomic start and stop positions of this gene are 295.231 KB and 295.529 KB with a length of 0.298 KB. (8) The gene that has the name APES013. The genomic start and stop positions of this gene are 295.342 KB and 295.518 KB with a length of 0.177 KB. (9) The gene that has the name APES014. The genomic start and stop positions of this gene are 295.572 KB and 296.676 KB with a length of 1.104 KB. (10) The gene that has the name APE0419. The genomic start and stop positions of this gene are 296.676 KB and 295.891 KB with a length of 0.786 KB. (11) The gene that has the name APE0420. The genomic start and stop positions of this gene are 297.071 KB and 298.857 KB with a length of 1.786 KB. (12) The gene that has the name APE0422. The genomic start and stop positions of this gene are 297.993 KB and 297.448 KB with a length of 0.546 KB. (13) The gene that has the name APE0423 and with a COG identifier of COG0084. The genomic start and stop positions of this gene are 298.857 KB and 298.099 KB with a length of 0.759 KB. (14) The gene that has the name APE0424. The genomic start and stop positions of this gene are 298.856 KB and 305.941 KB with a length of 7.085 KB. (15) The gene that has the name APE0425. The genomic start and stop positions of this gene are 299.332 KB and 298.973 KB with a length of 0.360 KB. (16) The gene that has the name APE0426 and with a COG identifier of COG2246. The genomic start and stop positions of this gene are 299.481 KB and 300.602 KB with a length of 1.122

KB. (17) The gene that has the name APE0427 and with a COG identifier of COG1573. The genomic start and stop positions of this gene are 300.649 KB and 301.296 KB with a length of 0.648 KB. (18) The gene that has the name APE0428 and with a COG identifier of COG1750. The genomic start and stop positions of this gene are 303.153 KB and 301.243 KB with a length of 1.911 KB. (19) The gene that has the name APE0429. The genomic start and stop positions of this gene are 303.244 KB and 303.786 KB with a length of 0.543 KB. (20) The gene that has the name APE0430. The genomic start and stop positions of this gene are 303.720 KB and 303.403 KB with a length of 0.318 KB. (21) The gene that has the name APE0431. The genomic start and stop positions of this gene are 303.833 KB and 304.911 KB with a length of 1.079 KB. (22) The gene that has the name APE0432. The genomic start and stop positions of this gene are 304.688 KB and 304.284 KB with a length of 0.405 KB. (23) The gene that has the name APE0434. The genomic start and stop positions of this gene are 305.005 KB and 305.611 KB with a length of 0.607 KB. (24) The gene that has the name APE0436 and with a COG identifier of COG1093. The genomic start and stop positions of this gene are 305.941 KB and 305.192 KB with a length of 0.750 KB. (25) The gene that has the name APES015 and with a COG identifier of COG2051. The genomic start and stop positions of this gene are 306.121 KB and 308.859 KB with a length of 2.738 KB. (26) The gene that has the name APES016 and with a COG identifier of COG1631. The genomic start and stop positions of this gene are 306.550 KB and 306.359 KB with a length of 0.192 KB. (27) The gene that has the name APE0437. The genomic start and stop positions of this gene are 308.859 KB and 306.674 KB with a length of 2.186 KB. (28) The gene that has the name APE0439. The genomic start and stop positions of this gene are 307.209 KB and 307.841 KB with a length of 0.633 KB. (29) The

gene that has the name APES017. The genomic start and stop positions of this gene are 308.989 KB and 312.190 KB with a length of 3.201 KB. (30) The gene that has the name APE0442 and with a COG identifier of COG1594. The genomic start and stop positions of this gene are 309.515 KB and 309.201 KB with a length of 0.315 KB. (31) The gene that has the name APES018. The genomic start and stop positions of this gene are 309.842 KB and 309.642 KB with a length of 0.201 KB. (32) The gene that has the name APE0443 and with a COG identifier of COG1761. The genomic start and stop positions of this gene are 310.223 KB and 309.915 KB with a length of 0.309 KB. (33) The gene that has the name APE0444 and with a COG identifier of COG3286. The genomic start and stop positions of this gene are 310.832 KB and 310.227 KB with a length of 0.606 KB. (34) The gene that has the name APE0445 and with a COG identifier of COG1096. The genomic start and stop positions of this gene are 312.190 KB and 310.912 KB with a length of 1.279 KB. (35) The gene that has the name APE0447 and with a COG identifier of COG1736. The genomic start and stop positions of this gene are 312.215 KB and 313.258 KB with a length of 1.043 KB. (36) The gene that has the name APE0448. The genomic start and stop positions of this gene are 312.650 KB and 313.258 KB with a length of 0.609 KB. (37) The gene that has the name APE0449 and with a COG identifier of COG0197. The genomic start and stop positions of this gene are 313.378 KB and 315.728 KB with a length of 2.350 KB. (38) The gene that has the name APE0450 and with a COG identifier of COG0303. The genomic start and stop positions of this gene are 313.995 KB and 315.728 KB with a length of 1.734 KB. (39) The gene that has the name APE0451. The genomic start and stop positions of this gene are 314.714 KB and 314.028 KB with a length of 0.687 KB. (40) The gene that has the name APES019. The genomic start and stop positions of this gene are 315.792 KB

and 318.996 KB with a length of 3.204 KB. (41) The gene that has the name APE0452. The genomic start and stop positions of this gene are 316.791 KB and 316.237 KB with a length of 0.555 KB. (42) The gene that has the name APE0453. The genomic start and stop positions of this gene are 316.247 KB and 317.576 KB with a length of 1.330 KB. (43) The gene that has the name APE0454 and with a COG identifier of COG1489. The genomic start and stop positions of this gene are 317.542 KB and 316.820 KB with a length of 0.723 KB. (44) The gene that has the name APE0456. The genomic start and stop positions of this gene are 318.099 KB and 317.632 KB with a length of 0.468 KB. (45) The gene that has the name APE0457 and with a COG identifier of COG0160. The genomic start and stop positions of this gene are 317.638 KB and 318.996 KB with a length of 1.359 KB. (46) The gene that has the name APE0458. The genomic start and stop positions of this gene are 318.432 KB and 318.914 KB with a length of 0.483 KB. (47) The gene that has the name APE0459. The genomic start and stop positions of this gene are 319.335 KB and 319.673 KB with a length of 0.339 KB. (48) The gene that has the name APE0460. The genomic start and stop positions of this gene are 319.733 KB and 324.526 KB with a length of 4.793 KB. (49) The gene that has the name APE0461 and with a COG identifier of COG1591. The genomic start and stop positions of this gene are 320.272 KB and 320.703 KB with a length of 0.432 KB. (50) The gene that has the name APE0462 and with a COG identifier of COG1855. The genomic start and stop positions of this gene are 322.241 KB and 320.700 KB with a length of 1.542 KB. (51) The gene that has the name APE0463. The genomic start and stop positions of this gene are 321.610 KB and 322.074 KB with a length of 0.465 KB. (52) The gene that has the name APE0464. The genomic start and stop positions of this gene are 322.317 KB and 323.228 KB with a length of 0.912 KB. (53) The gene that has the name APE0465 and

with a COG identifier of COG0301. The genomic start and stop positions of this gene are 324.526 KB and 323.288 KB with a length of 1.239 KB. (54) The gene that has the name APE0466. The genomic start and stop positions of this gene are 324.030 KB and 324.335 KB with a length of 0.306 KB. (55) The gene that has the name APE0468. The genomic start and stop positions of this gene are 324.606 KB and 325.575 KB with a length of 0.969 KB. (56) The gene that has the name APE0469 and with a COG identifier of COG1318. The genomic start and stop positions of this gene are 325.141 KB and 325.575 KB with a length of 0.435 KB. (57) The gene that has the name APE0470 and with a COG identifier of COG1277. The genomic start and stop positions of this gene are 325.980 KB and 326.717 KB with a length of 0.738 KB.

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This connectron controls the turning off of the expression of the following connectron(s): (1) The connectron that has the identifier 220 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 284.009 KB and 284.071 KB with a length of 0.063 KB. (2) The connectron that has the identifier 221 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 284.144 KB and 284.073 KB with a length of 0.072 KB. (3) The connectron that has the identifier 222 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 284.073 KB and 284.145 KB with a length of 0.073 KB. (4) The connectron that has the identifier 225 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 284.251 KB and 284.158 KB with a length of 0.094 KB. (5) The connectron that has the identifier 226 is on chromosome 1 in the positive direction. The genomic start and stop positions of this

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connectron are 284.158 KB and 284.251 KB with a length of 0.094 KB. (6) The connectron that has the identifier 228 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 284.253 KB and 284.280 KB with a length of 0.028 KB. (7) The connectron that has the identifier 231 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 284.283 KB and 284.305 KB with a length of 0.023 KB. (8) The connectron that has the identifier 240 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 295.415 KB and 295.444 KB with a length of 0.030 KB. (9) The connectron that has the identifier 248 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 300.757 KB and 300.742 KB with a length of 0.016 KB. (10) The connectron that has the identifier 249 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 300.781 KB and 300.767 KB with a length of 0.015 KB. (11) The connectron that has the identifier 253 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 305.334 KB and 305.348 KB with a length of 0.015 KB. (12) The connectron that has the identifier 254 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 305.358 KB and 305.372 KB with a length of 0.015 KB. (13) The connectron that has the identifier 255 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 305.566 KB and 305.552 KB with a length of 0.015 KB. (14) The connectron that has the identifier 257 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 305.582 KB and 305.568 KB with a length of 0.015 KB. (15) The connectron that has the identifier 273 is on

chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 317.682 KB and 317.668 KB with a length of 0.015 KB. (16) The connectron that has the identifier 275 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 317.704 KB and 317.690 KB with a length of 0.015 KB. (17) The connectron that has the identifier 277 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 319.097 KB and 319.127 KB with a length of 0.031 KB. (18) The connectron that has the identifier 283 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 320.513 KB and 320.484 KB with a length of 0.030 KB. (19) The connectron that has the identifier 290 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 325.979 KB and 325.950 KB with a length of 0.030 KB. (20) The connectron that has the identifier 291 is on chromosome 1 in the positive direction. The genomic start and stop positions of this connectron are 325.950 KB and 325.979 KB with a length of 0.030 KB. (21) The connectron that has the identifier 294 is on chromosome 1 in the negative direction. The genomic start and stop positions of this connectron are 326.878 KB and 326.716 KB with a length of 0.163 KB.

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